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December 3, 2003, 18:57:14; Search time 33.75 Seconds (without alignments) 145.793 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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172
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	Description	Bovine G protein-c	Bowine pituitary-d	Bovine 19P2 ligand	Bovine pituitary-d	Bovine oxytocin se	19P2 ligand peptid	19P2 ligand peptid	Bovine CRH releasi	Bovine PrRP-31 pep
SUMMARIES	ID	AAW31371	AAW97218	AAW87613	AAW95188	AAB10347	AAY49290	AAY49298	AAG62516	AAE26399
	08	18	50	20	50	71	21	21	22	23
	Query Match Length DB ID	31	31	31	31	31	31	31	31	31
de	-	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
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31 24 ABUG0825 32 20 AAW31372 32 20 AAW31372 32 21 AAB10348 32 24 ABUG0831 33 22 AAGG2517 33 22 AAGG2517 33 21 AAW31373 33 22 AAGG2518 33 22 AAGG2518 33 22 AAW31373 34 22 AAGG2518 36 20 AAW31368 37 21 AAW31368 38 20 AAW31368 39 20 AAW31368 30 20 AAW31368 31 22 AAGG2522 31 22 AAGG2515 31 22 AAB90995 31 22 AAB90993 31 22 AAB90993 31 22 AAB90993 31 22 AAB90993 31 22 AAB90993 31 22 AAB90993 31 22 AAB90993	Peptide production Peptide production	C)	pituitary			, ,		pituitary	Bovine oxytocin se			Peptide production		Bovine G protein-c	Bovine genome-driv				Bovine oxytocin se	Bovine CRH releasi	Bovine CRH releasi	Prolactin releasin	bPrRp31 peptide, u	๋ข	type		Murine pituitary-d	Murine pituitary-d	Rat oxytocin secre	Rat prolactin-rele	19P2 ligand peptid	Rat CRH releasing	Prolactin releasin	PrrP	Peptide production	
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ALIGNMENTS

AAW31371 standard; Peptide; 31 AA AAW31371; RESULT 1 AAW3137

Bovine G protein-coupled receptor ligand peptide fragment 1.

(first entry)

06-APR-1998

G protein-coupled receptor; ligand binding; pharmaceutical; modulator; pituitary; central nervous system; pancreas; prophylactic; therapeutic_agent.

96JP-0246573. 95JP-0343371. 96JP-0059419. 96JP-0211805. 96WO-JP03821. 18-SEP-1996; 28-DEC-1995; 15-MAR-1996; 12-AUG-1996; 109724436-A2 26-DEC-1996; BOR Caurus. 10 JUL-1997

(TAKE) TAKEDA CHEM IND LTD

Fujii R, Fukusumi S, Habata Y, Hinuma S, Hosoya M; Kawamata Y, Kitada C;

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Matches
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This ligand could have specific applications as a prophylactic or therapeutic agent for dementia, depression, hyperkinetic syndrome, clisturbance of consciousness, anxiety syndrome, schizophrenia, trauma, growth hormone secretory disease, hyper- and polyphagia, hypercholesterolaemia, hyperdiyocridaemia, hyperlipidaemia, hyperlipidaemia, hyperprolactinaemia, diabetes, cancer, pancreatitis, renal disease, hyperprolactinaemia, anylotrophic lateral sclerosis, acute myocardial infarction, spinocerebellar degeneration, bone fracture, transient brain ischaemia, amylotrophic lateral sclerosis, acute myoracial infarction, spinocerebellar degeneration, bone fracture, transient brain ischaemia, amylotrophic lateral sclerosis, acute mydor oligogalactia. Assays can also be developed to screen compounds which are capable of altering the binding activity of the ligand thus capable contains the binding activity of the ligand thus
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                                        Ligand peptide for G protein-coupled receptor - acts by modulating function in the central nervous system, pancreas and pituitary gland
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                                                                                 Claim 2; Page 160; 258pp; English.
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             N-PSDB; AAV02394
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prolactinoma, infertility, impotence, amenorrhea, galactorrhea, acromegaly, Chiari-Frommel syndrome, Argonz-del Castilo syndrome, Probes-Albright syndrome, lymphoma, Sheehan syndrome or dyszoospermia. The inhibitory agents can also be used as contraceptives. The agents for modulating placental function can be used for treating or preventing choriocarcinoma, hydatid mole, irruption mole, abortion, unthrifty fetus, abnormal saccharometabolism, abnormal lipidmetabolism or oxytocia.
                                                                                                                                                                                                                                                                      The present sequence represents a bovine pituitary-derived ligand fragment. It is used in the course of the invention. The specification describes an agent for modulating prolactin secretion which comprises a ligand polypeptide or a salt, for a G protein-coupled receptor (GCCR) protein. The agents for promoting prolactin secretion can be used for treating or preventing hypocvarianism, gonecyst cacogenesis, menopausal syndrome, euthyroid or hypometabolism. They can by used for promoting lactation in a domestic mammal and as an aphrodisiac. The agents for inhibiting prolactin secretion can be used for treating or preventing pituitary adenomatosis, brain tumour, emmeniopathy, autoimmune disease,
                                                              Use of G protein-coupled receptor ligands - for modulating prolactin secretion or placental function, e.g. for treating menopausal syndrome, tumours, autoimmune disease or abnormal pregnancy
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100.0%; Pred. No. 1.1e-18;
ive 0; Mismatches 0;
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                                                                                                                                                                                                           Claim 3; Page 135; 241pp; English
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WPI; 1999-105614/09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pituitary-derived ligand polypeptide; G-protein coupled orphan receptor;
                                                                                                                                                                                   high doses) prolactin secretion-inhibiting properties.

High doses) prolactin secretion-inhibiting properties.

Used in the treatment and prevention of various diseases including: senile dementia, cerebrovascular dementia, and dementia associated with: genealogical disorders (e.g. Alaheimer's disease, Parkinson's disease, Pick's disease, Huntington's disease), infectious diseases.

C. Guerarfeld-Jakob's), endocrine or metabolic disease or toxicosis (e.g. hypothyroidism, vitamin B12 deficiency, alcoholism, intoxication by drugs, metal and organic compounds), tumourigenic continuation by drugs, metal and organic compounds), tumourigenic subarachnoidal heamorihage, and other types of demential, depression, hyperactive child syndrome (microencephalopathy) and disturbance of consciousness. It is also useful for prevention and treatment of disease associated with prolactin hypo and hypersecretion respectively, including: hypothrocactinaemia, pituitary adenoma, breast cancer, infertility, impotence and autoimmum disease.

C. (hypersecretion disorders), and seminal vesicle hypoplasia, osteoporosis, menopausal syndrome and renal failure (hyposecretion reagent for study of the prolactin secretory function or as a test
                      This is the amino acid sequence.

protein-coupled receptor ligand 19P2L. A method suitable for commercial high-level production of 19P2L comprises expressing the ligand in host cells as a recombinant fusion protein e.g. with human basic fibroblast growth factor (see AAV83792-93) that has been modified to include an N-terminal cysteine residue. The 11gand is released from the fusion by cyanylation followed by ammonolysis. 19P2L has prolactin secretion-stimulating and (at ammonolysis. 19P2L has prolactin factor inhibiting properties. It can be
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 31;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene therapy; transgenic animal; bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       lactogogue in mammalian farm animals.
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97JP-0109974.

28-APR-1997;

98WO-JP01923

27-APR-1998;

WO9849295-A1

05-NOV-1998.

(TAKE) TAKEDA CHEM IND LTD

Fukusumi S, Hinuma S;

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The invention relates to a murine pituitary-derived ligand polypeptide which is a ligand for the G-protein coupled orphan receptor designated CC which is a ligand for the G-protein coupled orphan receptor designated CFR10 (human) or URF-1 (rat). Cells transformed with a vector containing the ligand polypeptide encoding DNA are used to produce a recombinant containing the ligand polypeptide. The ligand polypeptide and can be used to screen for agents that modulate binding of the CC function of the ptulitary, central nervous system, pancreas and other clissues and can be used to screen for agents that modulate binding of the polypeptide to the receptor; to quantify the amount of receptor in a sample and to raise antibodies. They may also be used therapeutically, e.g. to treat senile demential Alzheimer's, Parkinson's or Huntington's disease; schizophrenia; disorders of growth hormone secretion; cancer; rheumatoid arthritis, epilepsy and many others, also to improve post-coperative nutritional status and as vasopressor. Transgenic animals carrying the ligand polypeptide encoding DNA or its mutein are used to disease, for drug screening and as source of cell lines. The ligand colypeptide expressing genes, as models of disease, for drug screening and as source of cell lines. The ligand cantisers, in drug development; for gene therapy and to develop transgenic animals. The present sequence represents a bovine genome-derived ligand colypeptide fragment which is similar to the murine ligand-polypeptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   treatment; disease; pain; atonic bleeding; uterine receptor protein; caesarean section; artificial fertilization; galactostasis; goat; pig; veterinary medicine; milk production.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                     protein coupled receptors - used
                     New polypeptide ligand for orphan G protein coupled receptors - for treating disorders of central nervous system, pituitary and
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                                                                                                               Example 19; Page 150; 206pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matsumoto H, Kitada C, Hinuma S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB10347 standard; peptide; 31 AA
                                                                           pancreas, and for drug screening
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tes 31; Conserva
WPI; 1999-009423/01.
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19P2 ligand peptide fragment
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                                                    Query Match
Best Local Similarity
Local Similarity
Local 31; Conservative
                                                                                                                                                                                                                                              (first entry)
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                                                                             This invention describes a novel oxytocin secretion-regulating agent which contains a ligand peptide or its salt for the g protein-coupled receptor protein. It is useful in the form of drugs for ameliorating, preventing and treating diseases relating to oxytocin secretion e.g. weak pains and atonic bleeding, before and after expulsion of placenta, uterine recovery failure, caesarean section, stoppage of artificial fertilization or galactostasis and is also applicable in veterinary medicine for promoting milk production in cow, goat and pig. This sequence represents a bovine peptide which acts as an oxytocin secretion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention provides a monoclonal antibody which has a specific reaction with the part peptide of the C-terminal of 19P2 ligand or its derivative. The antibodies can be used in diagnosis or to treat or prevent diseases associated with abnormality in the pituitary function regulatory mechanism (e.g. promotion of prolactin secretion), central nervous regulatory mechanism, and pancreatic function regulatory
Physiologically-active polypeptide recognized as ligand by G
protein-coupled receptor protein, for promoting secretion of oxytocin, as drugs for diseases relating to oxytocin secretion and in veterinary
                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Monoclonal antibody, 19P2 ligand, diagnosis, prolactin secretion,
pituitary, regulatory mechanism, central nervous system; pancreatic.
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100.0%; Pred. No. 1.1e-18;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New monoclonal antibodies, useful in diagnosis, studying diseases related to ligand abnormality
                                                                                                                                                                                                                                                                                 1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31
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                                                                                                                                                                                                                                                                                                                                                                     AAY49290 standard; peptide; 31 AA
                                                         Claim 3; Page 50; 72pp; Japanese
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                                                                                                                                                                                                                                                                                                                                                                                                                                        19P2 ligand peptide fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99WO-JP02650.
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                                                                                                                                                                                                              Sequence
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                                   medicine
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mechanism. The antibody-based immunoassay can also be applied in clarifying the physiological functions of the ligand and its derivative. Sequences AAY49290-302 represent peptide fragments of the 1992 ligand.
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Pred. No. 1.1e-18;
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100.0%; Pred. No. ...
0; Mismatches
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17-MAY-2001; 2001JP-0147341.
                                                                        17-AUG-2001, 2001US-0932161
                                                                                            28-APR-2000; 2000US-0560915
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                                                                                                                                                Civelli O, Lin S;
                                                                                                                (CIVE/) CIVELLI O.
                              US2002037533-A1.
                                                                                                                             (LINS/) LIN S.
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          Bos taurus.
                                                                                                                                                                                                                            antagonist
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                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence describes a method of controlling the secretion of corticotrophin releasing hormone (CRH), involving the use of a G protein receptor This can be used to control the secretion of CRH and is useful as an analgesic or for treating, preventing or ameliorating diseases associated with CRH secretion such as hyperaldosteronism, hypercortisolaemia, secondary or chronic hypoaremocorticism, Addison's disease (including boredom, nausee, pigmentation, hypogonadism, hair loss, and hypotension), adread gland hypofunction and obesity. The present sequence is a peptide used in the exemplification of the
                                                                                                              Cow; corticotrophin releasing hormone; CRH; G protein receptor ligand; analgesic; hyperaldosteronism; hypercortisolaemia; hypoadrenocorticism; Addlson's disease; adrenal gland hyperfunction; obesity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wakefulness; sleep disorder; prolactin releasing peptide receptor; PrRP; GPR10; therapy; epilepsy; narcolepsy; sleepiness; sleep apnoea; insomnia; idiopathic hypersomnia; psychogenic hypersomnia; seizure; anticonvulsant; bovine.
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                                                                                                                                                                                                                                                                                                                                                Use of G protein receptor ligand or peptide for controlling
                                                                                            Bovine CRH releasing protein related peptide SEQ ID NO: 3.
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                                                                                                                                                                                                                                                                                                                                                            corticotropin releasing hormone secretion
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                             AAG62516 standard; peptide; 31 AA.
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                                                                                                                                                                                                                                                                                                     Matsumoto H, Hinuma
                                                                                                                                                                                                                           17-NOV-2000; 2000WO-JP08119.
                                                                                                                                                                                                                                                                               (TAKE ) TAKEDA CHEM IND LTD.
                                                                                                                                                                                                                                               18-NOV-1999; 99JP-0327900
26-SEP-2000; 2000JP-0297073
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                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bovine PrRP-31 peptide.
                                                                                                                                                                                                                                                                                                                           WPI; 2001-355552/37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31 AA;
                                                                                                                                                                               WO200135984-A1.
                                                                        24-AUG-2001
                                                                                                                                                                                                     25-MAY-2001
                                                                                                                                                          Bos taurus
                                                                                                                                                                                                                                                                                                     Kitada C,
                                                 AAG62516;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAE26399;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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The present invention relates to a method of screening for compounds for promoting wakefulness or sleep in a mammal. The method involves administering a prolactin releasing peptide (PrRP) receptor (GPR10) agonist or antagonist respectively and determining the ability of the compound to promote wakefulness or sleep. The compounds identified compound to promote wakefulness or sleep. The compounds identified associated with absence seizures and in promoting wakefulness and sleep in individuals having sleep disorders such as insomnia and narcolepsy. Prep receptor agonists may be used to treat common disorders which lead to sleepiness, e.g. sleep appose, narcolepsy, idiopathic hypersomnia and psychogenic hypersomnia. PrRP receptor antagonists are useful for promoting sleep and for treating insomnia such as adjustment sleep disorder and psychophysiologic insomnia. The present sequence is bovine prRP-31 peptide.
Screening for compounds useful for promoting wakefulness or sleep, and for treating sleeping disorders, e.g. insomnia, hypersomnia or sleep apnea, comprises administering a prolactin releasing peptide agonist or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peptide production by gene recombination associated peptide #9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 172; DB 23; Length 31; 100.0%; Pred. No. 1.1e-18;
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                                                                                                                                                                                                                    Disclosure; Page 24; 35pp; English.
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                                                                                                                                          The invention describes a method of producing a peptide comprising the excision of the N and C-terminals of a target peptide with enzymes or chemically through the attached cleavage sites repeated by ligation in a precursor protein. The method is for producing (low-molecular) peptides e.g. KiSS-1 peptide and GRP8 ligand for subsequent applications by the gene recombination technique through tandem repeats to provide a precursor protein with specific cleavage sites. With this method, peptide production can be carried out easily to provide large quantities of the required peptides. This is the amino acid sequence of a peptide associated with the peptide production method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention describes a method of producing a peptide comprising the excision of the N and C-terminals of a target peptide with enzymes or chemically through the attached cleavage sites repeated by ligation in a
                                                                            Process for producing peptides e.g. KiSS-1 peptide and GPR8 ligand for subsequent applications by gene recombination technique through tandem repeats to provide precursor protein with specific cleavage sites -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Process for producing peptides e.g. KiSS-1 peptide and GPR8 ligand for subsequent applications by gene recombination technique through tandem repeats to provide precursor protein with specific cleavage sites -
                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peptide production by gene recombination associated peptide #15.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 production; low-molecular peptide; KiSS-1; GPR8 ligand;
                                                                                                                                                                                                                                                                                               Length 31;
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                                                                                                                                                                                                                                                                                              100.0%; Score 172; DB 24; 100.0%; Pred. No. 1.1e-18;
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                                 Kitada C;
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                                                                                                                                                                                                                                                                                                                     Mismatches
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                                                                                                                      Disclosure; Page 58; 87pp; Japanese.
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                                 Ito T,
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          (TAKE ) TAKEDA CHEM IND LTD
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                              Nishimura O, Suenaga M,
                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2003-129302/12.
                                                      WPI; 2003-129302/12.
                                                                                                                                                                                                                                                                                                       Local Similarity
es 31; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene recombination
                                                                                                                                                                                                                                                                        31 AA;
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                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                               ABU60831;
                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peptide
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                                                                                                                                                                                                                                                                                                                     Matches
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This sequence represents a peptide fragment of a novel bovine pituitary derived ligand corresponding to amino acid residues 23 to 54 of the sequence in AAW31368 and is used in an assay to monitor ligand binding to the G protein-coupled receptor protein. Pharmaceutical compositions containing this ligand may be used as a pituitary function modulator. The second have specific applications as a prophylactic or the rapeutic agent for dementia, depression, hyperkinetic syndrome, disturbance of consciousness, anxiety syndrome, soffizophrenia, trauma, hypercholesterolaemia, hyperglyceridaemia, hyperlipidaemia, trauma, hyperprolactinaemia, disbetes, cancer, pancreatitis, renal disease, hyperprolactinaemia, disbetes, cancer, pancreatitis, renal disease, hyperprolactinaemia, disbetes, cancer, pancreatitis, renal disease, Turner's syndrome, neurosis, rematcid arthritis, spinal injury, transient brain ischaemia, amylotrophic lateral sclerosis, acute
precursor protein. The method is for producing (low-molecular) peptides egg. K188-1 peptide and GPRB ligand for subsequent applications by the gene recombination technique through tandem repeats to provide a precursor protein with specific cleavage sites. With this method, epptide production can be carried out easily to provide large quantities of the required peptides. This is the amino acid sequence of a peptide associated with the peptide production method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         G protein-coupled receptor; ligand binding; pharmaceutical;
modulator; pituitary; central nervous system; pancreas; prophylactic;
                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                     Length 31;
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                                                                                                                                                                                                                                                                                                                     100.0%; Score 172; DB 24; 100.0%; Pred. No. 1.1e-18;
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0; Mismatches
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95JP-0343371.
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                                                                                                                                                                                                                                                                                                                                                                                    31; Conservative
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N-PSDB; AAV02395.
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                                                                                                                                                                                                                                                                                                                                                      Local Similarity
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                                                                                                                                                                                                                                                          31 AA;
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28-DEC-1995;
15-MAR-1996;
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                                                                                                                                                                                                                                                             Sequence
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                                                                                                                                                                                                                                                                                                                        Query Match
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Matches
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disease, for drug screening and as source of cell lines. The ligand polypeptide DNA is used as a source of probes and primers; to identify related sequences; in receptor-binding assays; for production of Ab and antisera; in drug development; for gene therapy and to develop transgenic animals. The present sequence represents a bovine genome-derived ligand polypeptide fragment which is similar to the murine ligand-polypeptide.

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Gapa

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Indels

Length 32;

100.0%; Score 172; DB 20; 100.0%; Pred. No. 1.2e-18;

0; Mismatches

31, Conservative

Similarity

Best Local

Matches

32 AA;

Sequence Query Match

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us-09-868-885b-3.rag

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The invention relates to a murine pituitary-derived ligand polypeptide which is a ligand for the G-protein coupled orphan receptor designated GPRIO (human) or URLA: (rat). Cells transformed with a vector containing the ligand polypeptide encoding DNA are used to produce a recombinant ligand polypeptide. The ligand polypeptide, and its fragments, modulate ligand polypeptide. The ligand polypeptide is sorient for agents that modulate binding of the polypeptide to the receptor; to agents that modulate binding of the polypeptide to the receptor; to quantify the amount of receptor in a sample and to raise antibodies. They may also be used therapeutically, e.g. to treat senile dementia; Alzhehmer's, Parkinson's or Huntington's diseases; Creuzfeld-Jakob disease; poisoning by heavy metals or drugs; diabetes; schizophrenia; disorders of growth hormone secretion; cancer; rheumatoid arthritis, epilepsy and many others, also to improve postroperative nutritional status and as vasopressor. Transgenic animals carrying the ligand polypeptide encoding DNA or its mutein are used to study the function of the polypeptide-expressing genes, as models of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pituitary-derived ligand polypeptide; G-protein coupled orphan receptor; GPR10; UHR-1; modulator; pituitary; central nervous system; pancreas; tissue; screen; therapeutic; binding; senile dementia; ligand; murine; Alzheimer's disease; Parkinson's disease; Huntington's disease; drug; Creutzfeld-Jakob disease; polsoning; schizophrenia; growth hormone; secretion; diabetes; cancer; rheumatoid arthritis; epilepsy; vasopressor;
myocardial infarction, spinocerebellar degeneration, bone fracture, trauma, atopic dermatitis, osteoporosis, aethma, epilepsy, infertility and/or oligogalactia. Assays can also be developed to screen compounds which are capable of altering the binding activity of the ligand thus affecting activation of the G protein-coupled receptor protein.
                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                            100.0%; Score 172; DB 18; 100.0%; Pred. No. 1.2e-18;
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Best Local Similarity 100.
Matches 31; Conservative
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                                                                                                                                       Bovine, oxytocin secretion promoter; G protein-coupled receptor protein; treatment; disease; pain; atonic bleeding; uterine recovery failure; cow; caesarean section; artificial fertilization; galactostasis; goat; pig;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Physiologically-active polypeptide recognized as ligand by G protein-coupled receptor protein, for promoting secretion of oxytocin, as drugs for diseases relating to oxytocin secretion and in veterinary
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                                                                                                           Bovine oxytocin secretion promoting peptide SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 172; DB 21; 100.0%; Pred. No. 1.2e-18;
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                                                                                                                                                                                          veterinary medicine; milk production
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             AAB10348 standard; peptide; 32 AA
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                                                                           (first entry)
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nes 31; Conserv
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Matches
AAB10348
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The present sequence describes a method of controlling the secretion of corticotrophin releasing hormone (CRH), involving the use of a G protein receptor ligand. This can be used to control the secretion of CRH and is useful as an analgesic or for treating, preventing or ameliorating diseases associated with CRH secretion such as hyperaldosteronism, hypercortisolaemia, secondary or chronic hypoadremocorticism, Addison's disease (including boredom, nausea, pigmentation, hypogonadism, hair loss, and hypotension), adrenal gland hypofunction and obesity. The present sequence is a peptide used in the exemplification of the
                                                                                                                                                                                                                                     Cow, corticotrophin releasing hormone, CRH; G protein receptor ligand; analgesic; hyperaldosteronism; hypercortisolaemia; hypoadrenocorticism; Addison's disease; adrenal gland hyperfunction; obesity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Use of G protein receptor ligand or peptide for controlling corticotropin releasing hormone secretion -
                                                                                                                                                                                                         Bovine CRH releasing protein related peptide SEQ ID NO: 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             th 100.0%; Score 172; DB 22; Similarity 100.0%; Pred. No. 1.2e-18; 31; Conservative 0; Mismatches 0;
 SRAHOHSMEIRTPDINPAWYAGRGIRPVGRF 31
                Disclosure; Page 64; 90pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matsumoto H, Hinuma S;
                                                                                                           AAG62517 standard; peptide; 32 AA
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Local Similarity

Search completed: December 3, 2003, 19:11:24 Job time : 34.75 secs

38, Appl 39, Appl 45, Appl 134, App 137, App 137, Appl 29, Appl 9, Appl 61, Appl 61, Appl 81, Appl 9, Appl 61, Appl

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: TABABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,678A
FILING DATE: 26-JUN 1998
PRIOR APPLICATION NUMBER: JP 172118/1997
PILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Conlin, David G.
REGISTRATION NUMBER: 48466-342
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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                                                  US-08-776-971-48
US-09-421-208-38
US-09-421-208-38
US-09-421-208-39
US-09-776-971-45
US-08-776-971-145
US-08-776-971-137
US-09-105-678A-29
US-09-105-678A-29
US-09-105-678A-3
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US-09-421-208-43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 7, Application US/09105678A Patent No. 6103882 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 617-523-6440 INFORMATION FOR SEQ ID NO: 7: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 31 amino acids
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Sequence 31, Appli
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                            GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31
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US-09-421-200-31

US-09-421-200-31

US-09-105-678A-32

US-09-105-678A-33

US-09-105-678A-33

US-09-105-678A-33

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Maximum Match 100%
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Result

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Gaps

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Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS:
ADDRESSE: DIKE, BRONSTEIN, ROBERTS & CUSHWAN, LLP
STREET: 130 Water Street
CITY: BOSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
ADDRESSEB: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 31;
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COMPUTER: IBM compatible
CORPUTER: IBM compatible
CORPUTER: IBM compatible
SOFTWARE: FastESEQ for Windows Version 2.0
SOFTWARE: Version US/08/776,971B
FILING DATE: 0.6-1997
CLASSIFICATION NUMBER: PCT/JP96/03821
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: DP 7/34371
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: JP 8/59419
FILING DATE: 12-MAR-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: 12-MG-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: IB-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: COMIN, DAVIG G.
REGISTRATION NUMBER: 27,026
REGISTRATION NUMBER: 27,026
REGISTRATION NUMBER: 47176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.0%; Score 172; DB 3; Best Local Similarity 100.0%; Pred. No. 1.3e-19; Matches 31; Conservative 0; Mismatches 0;
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MOLECULE TYPE: protein

FRAGMENT TYPE: internal

SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-08-776-971-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 97, Application US/08776971B Patent No. 6228984 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 aming acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Habata, Yugo
Kawamata, Yuji
Hosoya, Masaki
Fujii, Ryo
Fukusumi, Shoji
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Hinuma, Shuji
                                                                                                                                                                ZIP: 02109
COMPUTER READABLE FORM:
                                                                         Boston
                                                                                                                                  COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: MA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JS-08-776-971-97
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Hogoya, Masaki
Pujii, Ryoo
Pukusumi, Shoji
Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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                                                                                                                                                                             Sequence 31, Application US/09105678A

Patent No. 610382
GENERAL INFORMATION:
APPLICANT: Suenaga, Masato
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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CITY: BUL
STATE: WAS
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,678A
FILING DATE: 26-JUN-1998
PRIOR APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATYORNEY/AGENT INFORMATION:
NAME: Conlin, David G
REGISTRATION NUMBER: 27,026
REFERENCE/COCKET NUMBER: 31.
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION:
TELECOMMUNI
   1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31
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Patent No. 6228984
GENERAL INFORMATION:
APPLICANT: Hinuma, Shuji
Habata, Yugo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                US-09-105-678A-31
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US-08-776-971-5
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Gaps

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100.0%; Score 172; DB 3; Length 31; 100.0%; Pred. No. 1.3e-19; tive 0; Mismatches 0; Indels
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APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Tanaka, Yoko
APPLICANT: Mishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSER: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/421,208
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/105,678
FILING DATE: 26-JUM-1998
APPLICATION NUMBER: JF 172118/1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 SRAHOHSMEIRTPDINPAWYAGRGIRPVGRF 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31
                                               APPLICATION NUMBER: JF 172118/1997
PILING DATE: 27-JUN-1997
ATTORNEY, AGENT INPORMATION:
NAME: CONJIN, David G.
REGISTRATION NUMBER: 27,026
REPRENCE/DOCKET NUMBER: 48466-342
TELECOMMUNICATION INPORMATION:
TELEPHONE: 617-523-3400
   US 09/105,678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 31, Application US/09421208
Patent No. 6258561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Conlin, David G.
REGISTRATION NUMBER: 27,026
REFRENCE/DOCKET NUMBER: 4846
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEPAK: 617-523-6440
                                                                                                                                                                                                                                                                                                         TELEPAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
APPLICATION NUMBER: US 0:
FILING DATE: 26-JUN-1998
APPLICATION NUMBER: JP 1<sup>-</sup>
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Best Local Similarity 100.0
Matches 31; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-421-208-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Boston
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TOPOLOGY: 1
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Patent No. 6258561
GENERAL INFORMATION:
APPLICANT: Standar, Masato
APPLICANT: Tanaka, Yoko
APPLICANT: Tanaka, Yoko
APPLICANT: Tanaka, Yoko
APPLICANT: Nathimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: ADS WATER Street
CITY: Boston
STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
      COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTESQ for Windows Version 2.0
SOFTWARE: PASTESQ for Windows Version DATA:
APPLICATION DATA:
APPLICATION NUMBER: DCT/JP96/03821
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: PP /343371
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: JP 8/5919
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: JP 8/21805
FILING DATE: 12-AUG-1996
APPLICATION NUMBER: JP 8/21605
FILING DATE: 12-AUG-1996
APPLICATION NUMBER: JP 8/21605
FILING DATE: 12-AUG-1996
ATTORNEY/AGRAT INFORMATION:
NAME: CONIIN, David G.
REGISTRATION NUMBER: 47176
TELECOMMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNI
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ZIP: 02109
COMPUTER READABLE FORM:
MEDIUTH TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/421,208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
100.0%; Score 172; DB 3;
Best Local Similarity 100.0%; Pred. No. 1.3e-19;
Matches 31; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31
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US-08-776-971-97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
ZIP: 02109
COMPUTER READABLE FORM:
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 5
US-09-421-208-7
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REFERENCE/DOCKET NUMBER: 48466-342
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MOLECULE TYPE: peptide
                                                                                                                                               TYPE: amino acid
STRANDEDNESS:
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Patent No. 638764

GRUERAL INFORMATION:
APPLICANT: Civelli, Olivier
APPLICANT: Civelli, Olivier
APPLICANT: Lin, Steven
TILLE OF INVENTION: Therapeutic Compositions and Methods
TILLE OF INVENTION: Relating To Prolactin Releasing Peptide (PrRP)
TILLE OF INVENTION: WHORER: US/09/560,915
CURRENT APPLICATION UNMBER: US/09/560,915
CURRENT FILING DATE: 2000-04-28
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 13
LENGTH: 31
TYBE: PRT
CRANISM: Bos taurus
US-09-560-915-13
                                                                                                              Gaps
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US-09-105-678A-12

Sequence 32, Application US/09105678A

Sequence 32, Application US/09105678A

Patent No. 6103882

GENERAL INFORMATION:

APPLICANT: Suenaga, Masato

APPLICANT: Tanaka, Yoko

APPLICANT: Mishimura, Osamu

TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND

NUMBER OF SEQUENCES: 52

CORRESPONDENCE ADDRESS:

ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP

STREET: 130 Water Street

CITY: Boston

STATE: MA

COUNTRY: USA
                                                             ch 100.0%; Score 172; DB 3; Length 31; l. Similarity 100.0%; Pred. No. 1.3e-19; 31; Conservative 0; Mismatches 0; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,678A
FILING DATE: 26-UN-1998
                                                                                                                                                                              SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31
                                                                                                                                                    1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Conlin, David G.
REGISTRATION NUMBER: 27,026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31; Conservative
  peptide
                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
; MOLECULE TYPE:
US-09-421-208-31
                                                                                                                                                                                                                                                                           US-09-560-915-13
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Hosoya, Masaki
Pujii, Ryo
Fukusumii, Shoji
Fukusumii, Shoji
Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS:
ADDRESSE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                          Query Match
100.0%; Score 172; DB 3; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.3e-19;
Matches 31; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER KEALABLE FORM:
COMPUTER: DISKette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06-Feb-1997
CLASSIFTCATION: CURROWN:
APPLICATION DATA:
PRIONG DATE: 28-DEC-1996
APPLICATION NUMBER: JP 7/34371
FILING DATE: 12-MAR-1996
APPLICATION NUMBER: JP 8/59419
FILING DATE: 12-MG-1996
APPLICATION NUMBER: JP 8/59419
FILING DATE: 12-MG-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-MG-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-MG-1996
APPLICATION NUMBER: JP 8/21673
FILING DATE: 18-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31
                                                                                                                                                                                                                                                                                                                                                                                                                       1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Conlin, David G.
REGISTRATION NUMBER: 27,026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 6, Application US/08776971B Patent No. 6228984 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEPAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Hinuma, Shuji
Habata, Yugo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
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amino acid
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                                                                                                                                                                                                                                                                                           Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-105-678A-33
                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-776-971-7
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                                                                                                                                                                                                                Gaps
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                                                                                                                                                                        Length 32;
                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                                                                                                                                                                                                        Sequence 32, Application US/09421208
Patent No. 6558561
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CONDUTER EADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BEN FC compatible
COMPUTER: Floppy disk
COMPUTER: BEN FC compatible
OPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN BATA:
APPLICATION NUMBER: US/09/421,208
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/105,678
FILING DATE: 26-JUN-1998
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: COMIN, DAVIG G.
REGISTRATION NUMBER: 27,026
REGISTRATION NUMBER: 27,026
                                                                                                                                                              Query Match
100.0%; Score 172; DB 3;
Best Local Similarity 100.0%; Pred. No. 1.3e-19;
Matches 31; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
100.0%; Score 172; DB 3;
Best Local Similarity 100.0%; Pred. No. 1.3e-19;
Matches 31; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SRAHOHSMEIRTPDINPAWYAGRGIRPVGRF 31
                                                                                                                                                                                                                                                     1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31
                                                                                                                                                                                                                                                                                           1 SRAHOHSMEIRTPDINPAWYAGRGIRPVGRF 31
TYPE: amino acid
STRANDEDNESS: single
TOPOLGY: linear
MOLECULE TYPE: procein
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-08-776-971-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48466
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-3440
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 130 Water Street
CITY: Boston
STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; MOLECULE TYPE: peptide US-09-421-208-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
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02109
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                                                                                                                                                                                                                                                                                                                                                                          US-09-421-208-32
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                                                                                                                                                                                                                                                                                                                                                     RESULT 10
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inc.01-10;-(704-3)

inc.01-10;-(704-3)

inc.01-10;-(704-3)

sequence No. 6(10302)

sequence No. 144-13;

sequence
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ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 33;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
COMPUTER: IBM compatible
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASISEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06-Feb-1997
CLASSIPICATION AUCHORN
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP96/03821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Score 172; DB 3;
; Pred. No. 1.4e-19;
0; Mismatches 0;
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APPLICATION NUMBER: JP 7/34331
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: JP 8/59419
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-AUG-1996
FILING DATE: 12-AUG-1996
FILING DATE: 18-SEP-1996
                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/105,678
FILING DATE: 26-JUN-1998
APPLICATION NUMBER: UF 172118/1997
FILING DATE: 27-JUN-1997
ATTONEY, ACREAT INFORMATION:
NAME: CONLIN, DAVIG G.
REGISTRATION NUMBER: 27,026
REGISTRATION NUMBER: 27,026
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
APPLICATION NUMBER: US/09/421, 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/08776971B Patent No. 6228984 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.0%;
Matches 31; Conservative 0;
                                                                                                                                                                                                                                                                                                                   TELEFAX: 617-523-6440
INPORMATION FOR SEQ ID NO: 33:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Hinuma, Shuji
Habata, Yugo
                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 33 amino acida
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-421-208-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: MA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JS-08-776-971-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Tanaka, Yoko
APPLICANT: Tanaka, Yoko
APPLICANT: Manimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: 130 Water Street
CITY: Boston
STRET: MA
COUNTRY: USA
ZIP: 02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                              MEDIUM TYPE: DBRACHE
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FasESEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/776,971B
FILING DAYE: OS-Feb-1997
CLASSIFICATION NUMBER: UF/JP96/03821
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: JP 7/443371
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: JP 8/59419
FILING DATE: 18-MAR-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-AUG-1996
APPLICATION NUMBER: JP 8/21805
FILING DATE: 12-AUG-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: 12-AUG-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-REP-1996
ATTORNEY/AGENT INFORMATION:
NAME: CONLIN, DAVIG G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 47176
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-08-776-971-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: UZIUZ
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMpatible
COMPUTER: PSYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 33, Application US/09421208
Patent No. 6258561
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 617-523-6440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS
                       ZIP: 02109
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-421-208-33
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Gaps
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Kawanata, Yuji
Hosoya, Masaki
Fujii, Ryo
Fukusumi, Shoji
Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
CORRESPONDENCES: 140
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Hosoya, Masaki
Pujii, Nasaki
Pujii, Shoji
Pukusumi, Shoji
Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.0%; Score 172; DB 3; Length 98; Best Local Similarity 100.0%; Pred. No. 5.1e-19; Matches 31; Conservative 0; Mismatches 0; Indels
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COMPUTER: 1BM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASESEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06-Feb-1997
CLASSIFICATION: <unimal color of the color
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FILING DATE: 28-DEC-1996
APPLICATION NUMBER: DF 7/34331
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: JP 8/59419
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: JP 8/21605
FILING DATE: 18-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: CONLIN, DAVID G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 27,026
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 53
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                                    RAME: Conlin, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 47176
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: anino acids
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-08-776-971-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 44, Application US/08776971B
Patent No. 6228984
GENERAL INFORMATION:
APPLICANT: Hinuma, Shuji
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Habata, Yugo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 02109
COMPUTER READABLE FORM:
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COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 15
US-08-776-971-44
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Sequence 96, Appl
Sequence 26, Appl
Sequence 15, Appl
Sequence 15, Appl
Sequence 16, Appl
Sequence 16, Appl
Sequence 16, Appl
Sequence 43, Appl
Sequence 41, Appl
Sequence 17, Appl
Sequence 17, Appl
Sequence 17, Appl
Sequence 17, Appl
Sequence 18, Appl
Sequence 19, Appl
Sequence 2, Appli
Sequence 2, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 44, Appli
Sequence 3, Appli
Sequence 44, Appli
Sequence 44, Appli
Sequence 44, Appli
Sequence 44, Appli
Sequence 4, Appli
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Sequence 13, Application US/09932161

RENERAL INFORMATION:
APPLICANT: Civelli, Olivier

TILE OF INVENTION: Screening and Therapeutic Methods For TILE OF INVENTION: Promoting Wakefulness and Sleep;
TILE REPRENCE: P-UC 4679
CURRENT FILIAD DATE: 2001-08-17

PRIOR FILIAG DATE: 2000-04-28

NUMBER OF SEQ ID NOS: 24

SOCTWARE: PastSEQ for Windows Version 4.0

LENGTH: 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-044-592-9
US-10-108-915-30
US-09-738-626-4642
US-09-911-842-4
US-10-150-821-4
4 US-10-044-592-96

4 US-10-044-592-1

4 US-10-044-592-96

4 US-10-044-592-26

US-09-932-161-15

US-09-932-161-15

4 US-10-046-592-92

4 US-10-044-592-92

4 US-10-044-592-44

US-10-044-592-44

US-10-044-592-44

US-10-044-592-44

US-10-044-592-44

US-10-044-592-64

US-10-044-592-777-118
                                                                                                                                                                                                                                                                                        US-10-044-592-8
US-10-301-822-197
US-09-820-155-4
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                                                                                                                                                                                                                                                                                                                                                                                                                             ALIGNMENTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 2
US-10-096-777-13
; Sequence 13, Application US/10096777
; Publication No. US20030171270A1
; GENERAL INFORMATION:
; APPLICANT: Civelli, Olivier
; APPLICANT: Lin, Steven
                                                                                                                                                                                                                                                                                                      465
10
209
417
3594
3594
  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tryPE: PRT
CORGANISM: Bos taurus
US-09-932-161-13
  JS-09-932-161-13
  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 1
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                                                                                        December 3, 2003, 19:11:30 ; Search time 22.5 Seconds (without alignments) 256.244 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Description
                                                                                                                                                                                                                                                                                                                                                                              Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/USO9C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/USO9C_PUBCOMB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/USO9C_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/USO0C_PUBCOMB.pep:*
15: /cgn2_6/ptodata/1/pubpaa/USO0C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/USOOC_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/USOOC_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/USOOC_PUBCOMB.pep:*
17: /cgn2_6/ptodata/1/pubpaa/USOOC_PUBCOMB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/USOOC_PUBCOMB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/USOOC_PUBCOMB.pep:*
                GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                       1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31
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US-10-046-777-13

US-10-044-592-39

US-10-044-592-28

US-10-044-592-28

US-10-044-592-28

US-10-044-592-84

US-10-044-592-84

US-10-044-592-86

US-10-044-592-86

US-10-044-592-86

US-10-044-592-86

US-10-044-592-86

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US-10-044-592-86

US-10-044-592-86

US-10-044-592-86
                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                       684280 seqs, 185983659 residues
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                                                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                  OM protein - protein search, using sw model
                                                                                                                                                                                                 BLOSUM62
Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
                                                                                                                                             US-09-868-885B-3
172
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Perfect score:
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TITLE OF INVENTION: POLypeptides, their Production and Use
FILE REPERENT 2463192P
CURRENT APPLICATION NUMBER: US/10/044,592
CURRENT FILING DATE: 2002-01-10
PRIOR APPLICATION NUMBER: US/403639
PRIOR PLILOR DATE: 1999-25-10
PRIOR PLILOR DATE: 1999-25-10
PRIOR PLILOR DATE: 1999-25-10
PRIOR PLILOR DATE: 1999-25-10
PRIOR FILING DATE: 1997-04-28
NUMBER: OF SEQ ID NOS: 96
SEQ ID NO 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Hinuma, Shuji
APPLICANT: Hinuma, Shuji
APPLICANT: Eukusumi, Shoji
TITLE OF INVENTION:
FILE REPERENCE: 2463US2P
CURRENT APPLICATION NUMBER: US/10/044,592
CURRENT PILING DATE: 2002-01-10
PRIOR APPLICATION NUMBER: US 09/403639
PRIOR APPLICATION NUMBER: US 09/403639
PRIOR FILING DATE: 1999-04-27
PRIOR FILING DATE: 1990-04-27
PRIOR FILING DATE: 1990-04-27
PRIOR FILING DATE: 1990-04-27
PRIOR FILING DATE: 1990-04-28
NUMBER OF SEQ ID NOS: 96
SEQ ID NO 28
                                                                                                                                                                                                                                         Length 32;
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11arity 100.0%; Pred. No. 8.5e-18;
Conservative 0; Mismatches 0;
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100.0%; Pred. No. 8.7e-18;
tive 0; Mismatches 0;
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  PRIOR APPLICATION NUMBER: JP 9-109974
PRIOR FILING DATE: 1997-04-28
NUMBER OF SEQ ID NOS: 96
SOFTWARE:
SEQ ID NO 40
LENGTH: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-044-592-41
Sequence 41, Application US/10044592
Publication No. US20020143152A1
GENERAL INFORMATION:
APPLICANT: Hinuma, Shuji
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence 28, Application US/10044592
publication No. US20020143152A1
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Best Local Similarity 100.0
Matches 31; Conservative
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Best Local Similarity
Matches 31; Conserv
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; ORGANISM: Bovine
US-10-044-592-41
                                                                                                                                            TYPE: PRT
ORGANISM: Bovine
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TITLE OF INVENTION: Therapeutic Compositions and Methods
TITLE OF INVENTION: Relating To Prolactin Releasing Peptide (PrRP)
FILE REFERENCE: P-UC 3534
CURRENT APPLICATION NUMBER: US/10/096,777
CURRENT FILING DATE: 2002-03-12
PRIOR PILING DATE: 2002-03-28
NUMBER OF SEQ ID NOS: 24
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 31
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US-10-044-592-40
is Sequence 40, Application US/10044592
is Bequence 40, Application US/10044592
is Publication No. US20020143152A1
is GENERAL INFORMATION:
is APPLICANT: HILLIAM: Shuji
is APPLICANT: FURNBUMI, Shuji
is TITLE OF INVENTION: Polypeptides, their Production and Use
is FILE REFERENCE: 24631032P
is CURRENT APPLICATION NUMBER: US/10/044,592
is CURRENT FILING DATE: 2002-01-10
is PRIOR PILING DATE: 1999-25-10
is PRIOR FILING DATE: 1999-25-10
is PRIOR FILING DATE: 1998-04-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Hinuma, Shuji
APPLICANT: Hinuma, Shuji
APPLICANT: Fukusumi, Shoji
TILE OF INVENTION Polypeptides, their Production and Use
FILE REFERENCE: 2463US2P
CURRENT APPLICATION NUMBER: US/10/044,592
CURRENT APPLICATION NUMBER: US/10/044,592
CURRENT APPLICATION NUMBER: US 09/403639
PRIOR FILING DATE: 1999-25-10
PRIOR FILING DATE: 1999-04-27
PRIOR PILING DATE: 1999-04-27
PRIOR PLING DATE: 1999-04-27
PRIOR PILING DATE: 1997-04-28
NUMBER OF SEQ ID NOS: 96
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                                                                                                                                                                                                                                                                                                                                                          Query Match 100.0%; Score 172; DB 12; Best Local Similarity 100.0%; Pred. No. 8.2e-18; Matches 31; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.0%; Score 172; D
Best Local Similarity 100.0%; Pred. No. 8.2
Matches 31; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 39, Application US/10044592 Publication No. US20020143152A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Bovine
US-10-044-592-39
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US-10-044-592-39
                                                                                                                                                                                                                                                                                                            US-10-096-777-13
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LENGTH: 31
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10-044-592-86

1 Sequence 86, Application US/10044592

1 Publication No. US20020143152A1

1 GRENEAL INFORMATION:

1 APPLICANT: Hinuma, Shuji

1 TITLE OF INVENTION: Polypeptides, their Production and Use

1 TITLE OF INVENTION: Polypeptides, their Production and Use

2 TITLE OF INVENTION: Polypeptides, their Production and Use

2 TITLE OF INVENTION: Polypeptides, their Production and Use

3 FILE REPRENCE: 2463US2P;

4 CURRENT FILING DATE: 2002-01-10

5 FRIOR APPLICATION NUMBER: US 09/403639

7 PRIOR PILING DATE: 1999-28-10

7 PRIOR APPLICATION NUMBER: PCT/JP98/01923

7 PRIOR PILING DATE: 1997-04-28

7 PRIOR FILING DATE: 1997-04-28

7 SOFTWARE:

7 SEQ ID NO 86

7 LENGTH: 98
                                                                                                                                                                                                                                                                                                                APPLICANT: Hinuma, Shuji
APPLICANT: Hinuma, Shuji
APPLICANT: Fukusumi, Shoji
ITILE OF INTENTION: POLYPeptides, their Production and Use;
FILE REPERBNCE: 24631929
CURRENT FILING DATE: 2002-01-10
PRIOR APPLICATION NUMBER: US 09/403639
PRIOR PILING DATE: 1999-25-10
PRIOR PILING DATE: 1999-25-10
PRIOR PILING DATE: 1999-25-10
PRIOR PILING DATE: 1999-64-27
PRIOR APPLICATION NUMBER: PCT/JP98/01923
PRIOR PILING DATE: 1999-04-27
PRIOR PILING DATE: 1997-04-28
NUMBER OF SEQ ID NOS: 96
SEQ ID NOS: 96
LENGTH: 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 172; DB 14; Length 98; 100.0%; Pred. No. 2.7e-17; tive 0; Mismatches 0; Indels
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    Length 98;
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1. Similarity 100.0%; Pred. No. 2.7e-17;
31; Conservative 0; Mismatches 0;
  100.0%; Score 172; DB 14;
100.0%; Pred. No. 2.7e-17;
ive 0; Mismatches 0;
                                                                                            1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31
                                                                                                                        23 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 53
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                                                                                                                                                                                                                         US-10-044-592-84; Sequence 84, Application US/10044592; Publication No. US20020143152A1; GENERAL INPORMATION:
Query Match
Best Local Similarity 100.4
Matches 31, Conservative
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Best Local Similarity
Matches 31; Conserva
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Best Local Similarity
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US-10-044-592-86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-044-592-84
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; Sequence 82, Application US/10044592
; Publication No. US202020143152A1
; GENERAL INPORMATION:
   APPLICANT: Hinuma, Shuji
; APPLICANT: Hinuma, Shuji
; TITLE OF INVENTION: POLYPEPTIGES, their Production and Use
; FILE REFERENCE: 2463US2P
; CURRENT APPLICATION NUMBER: US/10/044,592
; CURRENT FILING DATE: 1999-25-10
; PRIOR APPLICATION NUMBER: US 09/403639
; PRIOR APPLICATION NUMBER: US 09/403639
; PRIOR APPLICATION NUMBER: US 09/403639
; PRIOR FILING DATE: 1998-04-27
; PRIOR FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 96
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                                                                                                                   Length 98;
                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Hinuma, Shuji
APPLICANT: Hinuma, Shuji
APPLICANT: Hinuma, Shuji
TITLE OF TEXLSUBLICANT: Polypeptides, their Production and Use
FILE REFERENCE: 2463182P
CURRENT APPLICATION NUMBER: US/10/044,592
CURRENT PILING DATE: 2002-01-10
PRIOR APPLICATION NUMBER: US 09/403639
PRIOR FILING DATE: 1999-25-10
PRIOR FILING DATE: 1999-04-27
PRIOR FILING DATE: 1998-04-27
PRIOR FILING DATE: 1998-04-27
PRIOR FILING DATE: 1997-04-28
NUMBER OF SEQ ID NOS: 96
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                                                                                                                   100.0%; Score 172; DB 14; 100.0%; Pred. No. 2.7e-17;
                                                                                                                                                                                                                                            23 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 53
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                                                                                                                                                                                                               1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31
                                                                                                                                                                   Mismatches
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US-10-044-592-38
Sequence 38, Application US/10044592
Publication No. US20020143152A1
GENERAL INFORMATION:
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                                                                                                                      Query Match 100.
Best Local Similarity 100.
Matches 31; Conservative
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                            ; TYPE: PRT
; ORGANISM: Murine
US-10-044-592-28
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ORGANISM: Bovine
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; ORGANISM: Bovine
US-10-044-592-82
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US-10-044-592-82
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LENGTH: 98
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         LENGTH: 98
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Gaps

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APPLICANT: Lin, Steven
TITLE OF INVENTION: Therapeutic Compositions and Methods
TITLE OF INVENTION: Therapeutic Compositions and Methods
TITLE OF INVENTION: Therapeutic Composition Releasing Peptide (PrRP)
FILE REFERENCE: P-UC 3534
CURRENT APPLICATION NUMBER: US/10/096,777
CURRENT APPLICATION NUMBER: US/08/560,915
PRIOR PLING DATE: 2000-04-28
PRIOR PLING DATE: 2000-04-28
SOFTWARE: PASISEQ for Windows Version 4.0
SEQ ID NO 14
LENGTH: 31
TYPE: PRT
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**Publication Wo. US20020143152A1

**GENERAL INFORMATION:

**APPLICANT: Hinuma, Shuji

**APPLICANT: Hinuma, Shuji

**TILE NEFERRING: 2453U52B1

**TITLE OF INVENTION: Polypeptides, their Production and Use

**CURRENT APPLICATION NUMBER: US/10/044,592

**CURRENT FILING DATE: 1999-25-10

**PRIOR FILING DATE: 1999-25-10

**PRIOR FILING DATE: 1999-04-27

**PRIOR FILING DATE: 1999-04-27

**NUMBER: OF SEQ ID NOS: 96

**SEQ ID NO 4

**LEMOTATION NOMBER: 1997-04-28

**SEQ ID NO 5: 96

**LEMOTATION NOMBER: 1997-04-28

**LEMOTATION NOMBER: 1997-04-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 163; DB 14; Length 31;
Pred. No. 1.6e-16;
0; Mismatches 2; Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 94.8%; Score 163; DB 12; Length 31; Best Local Similarity 93.5%; Pred. No. 1.6e-16; Matches 29; Conservative 0; Mismatches 2; Indels
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Publication No. US20020143152A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Fulunua, Shuji
APPLICANT: Fulusual, Shoji
TITLE OF INVENTION: Polypeptides, their Production and Use
FILE REPERENCE: 2463US2P
CURRENT APPLICATION NUMBER: US/10/044,592
CURRENT PLING DATE: 2002-01-10
PRIOR APPLICATION NUMBER: US 09/403639
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Best Local Similarity 93.5%;
Matches 29; Conservative
                               APPLICANT: Civelli, Olivier
      GENERAL INFORMATION:
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US-10-096-777-14
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CURRENT APPLICATION NUMBER: US/10/044,592
CURRENT FILING DATE: 2002-01-10
PRIOR APPLICATION NUMBER: US 09/403639
PRIOR APLICATION NUMBER: CT/JP98/01923
PRIOR APLICATION NUMBER: PCT/JP98/01923
PRIOR FILING DATE: 1998-04-27
PRIOR FILING DATE: 1998-04-27
PRIOR FILING DATE: 1997-04-28
NUMBER OF SEQ ID NOS: 96
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Fatent No. US20020037533A1
GENERAL INFORMATION:
APPLICANT: Civelli, Olivier
APPLICANT: Lin, Steven
TITLE OF INVENTION: Promoting Wakefulness and Sleep
TITLE OF INVENTION: Promoting Wakefulness and Sleep
FILE REFERENCE: PuC 4679
CURRENT APPLICATION NUMBER: US/09/932,161
CURRENT FILING DATE: 2001-08-17
PRIOR PAPLICATION NUMBER: US 09/560,915
PRIOR PAPLICATION NUMBER: US 09/560,915
NUMBER OF SEQ ID NOS: 24
SOFUTANARE: PARESEQ for Windows Version 4.0
SEQ ID NO 14
LENGTH: 31
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23 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 53
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                                                                                                                                                                         Sequence 88, Application US/10044592; Publication No. US20020143152A1; GENERAL INFORMATION:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Bovine
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US-09-932-161-14
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GenCore version 5.1.6 (c) 1993 - 2003 Compugen Ltd. Copyright

- protein search, using sw model OM protein

Run on:

December 3, 2003, 19:05:30 ; Search time 10.5 Seconds (without alignments) 283.927 Million cell updates/sec

US-09-868-885B-3 172 1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31

Title: Perfect score:

Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

283308 seqs, 96168682 residues Searched:

Total number of hits satisfying chosen parameters:

283308

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	prolactin-releasin	hypothetical prote	Mg protoporphyrin	Sun/nucleolar prot	hypothetical prote	adenine deaminase-	hypothetical prote	transcription regu	rok family protein	hypothetical prote	probable magnesium	conserved hypothet	hypothetical prote	conserved hypothet		excinuclease ABC c				conserved hypothet	hypothetical prote		_	_	_		probable regulator	probable glutathio	hypothetical prote
SUMMARIES	ΩI	JC7607	AH2016	T50904	A82193	867150	C75580	A98137	AH2896	B97672	AH3166	T31462	F83376	T21075	B69009	811210	H69157	T47959	T33175	AH3361	AB2664 ,	A97446	876955	A87664	S76814	T47548	S73484	E91002	C83292	B70569
	th DB	83 2	•	•	03 2	•		73 2	308 2	•	••	••	•••	94 2	430 1	98 2	•	•	•••	•	393 2	•	128 2	26 2	•	•	82 2	••	220 2	14 2
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عد	Query Match	94.8	32.8	32.0	31.7	31.1	30.8	30.2	30.2	30.2	30.2	30.2	29.9	29.7	29.7	29.7	29.7	29.4	29.1	29.1	28.8	28.8	28.5	28.5	28.2	28.2	28.2	27.9	27.9	27.9
	Score	163	56.5	55	54.5	53.5	53	52	52	52	25	52	51.5	51	51	51	51	50.5	20	20	49.5	49.5	49	49	48.5	48.5	48.5	48	48	48
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hypothetical prote	hypothetical prote	acetoacetyl-CoA re	BamB protein - Sal	sensory box histid	protoporphyrin IX	excinuclease ABC c	ABC excinuclease s	excinuclease ABC c	protoporphyrin IX	magnesium chelatas					
T21648	T39098	JC7675	B38176	D87559	T07958	A71315	AH2762	G97543	AE2351	875000	S37310	S64721	871288	T01789	T07126
7	~	N	N	~	N	7	7	N	~	~	~	N	N	~	N
348	365	397	424	637	772	960	973	982	1328	1331	1379	1380	1381	1382	1383
_	o.	7.9	27.9	27.9	27.9	27.9	27.9	27.9	27.9	27.9	27.9	27.9	27.9	27.9	27.9
27.	27	N	•												
48 27.9	48 27			48	48	48	48	48	48	48	48	48	48	48	48

ALIGNMENTS

Cispecies: Rattus norvegicus (Norway rat)
Riversation: U76001
Riversation: U76001
Riversation: Riversation and characterization of the rat prolactin-releasing peptide gene: Musication and characterization of the rat prolactin-releasing peptide gene: Musication: Spleen: U76007; MUID:21092785; PMID:11178959
AiAccession: U776007
AiAccession: U776

C;Genetics: A;Gene: PrRP A;Introns: 33/1

Query Match 94.8%; Score 163; DB 2; Length 83; Best Local Similarity 93.5%; Pred. No. 6.9e-17; Matches 29; Conservative 0; Mismatches 2; Indels

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Gaps

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1 SRAHQHSMEIRTPDINPAWYAGRGIRBVGRF 31
22 SRAHQHSMETRTPDINPAWYTGRGIRPVGRF 52 ð g

hypothetical protein allie86 [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
C;Species: Nostoc sp. PCC 7120
C;Species: Nostoc sp. errain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C;Accession: AH2016
C;Accession: AH2016
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, DNA Res. 8, 205-213, 2001
A;Tille: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium An A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Status: preliminary

A,Molecule type: DNA A,Residues: 1.303 «KUR» A,Cross-references: GB:BA000019; PIDN:BAB78052.1; PID:g17135506; GSPDB:GN00179 A,Experimental source: strain PCC 7120 C,Genetics: A,Gene: all1686

DB 2; Length 303; 32.8%; Score 56.5; Query Match 1;

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hypothetical protein AGR L 109 [imported] - Agrobacterium tumefaciens (strain C58, Cere C; Species: Agrobacterium tumefaciens C; Species: Agrobacterium tumefaciens C; Species: Agrobacterium tumefaciens C; Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 18-Nov-2002 C; Accession: A98137 R; Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B. Science 294, 2332-2328, 2001 A; Edword Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tu A; Reference number: A97359; MUID:21608551; PMID:11743194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     adenine deaminase-related protein - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
C;Accession: C75580
C;Accession: C75580
R;White, O.; Bisen, J.A.; Heidelberg, J.F.; Hickey, B.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:AE001863; GB:AE001825; NID:g6460670; PIDN:AAF12376.1; PID:g64606
A;Experimental source: strain R1
                                                                                                                                                                                                                                                              A,Molecule type: DNA
A,Rosidues 1-176 «JAD»
A,Gross references: EMBL:275161; NID:g1420572; PID:e252411; PID:g1420573; GSPDB:GN00015
A,Experimental source: strain S288C
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A,Molecule type: DNA
A,Residues: 1-73 <KUR>
A,Cross-references: GB:AE007870; PIDN:AAK88619.1; PID:g15158338; GSPDB:GN00170
C;Date: 12-Jul-1996 #Bequence_revision 12-Jul-1996 #text_change 19-Apr-2002 C;Accession: 867150 R;Jauniaux, J.C.; Poirey, R. submitted to the Protein Sequence Database, July 1996 A;Reference number: 867143 A;Accession: 867150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 53.5; DE Pred. No. 2.3; 5; Mismatches
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Pred. No. 6.1;
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  177 ARALAHAPDVSRPORHRACGAGORRRPAGR 206
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Best Local Similarity 31.2%;
Matches 10; Conservative
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A;Map position: 15R
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Best Local Similarity 40.0°
Matches 12; Conservative
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A; Residues: 1-376 < WHI>
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                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Gene: MIPS: YOR253w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Accession: C75580
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A;Gene: DRA0268
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                                                                                                                                                                                                                                                                                                                                                                                                 Mg procoporphyrin methyl transferase [imported] - Rubrivivax gelatinosus G;Species: Rubrivivax gelatinosus G;Species: Rubrivivax gelatinosus G;Species: 21-011-2000 #sequence_revision 21-010-2000 #sequence_revision 21-010-2000 #text_change 02-Sep-2000 G;Accession: T50904 #s.Nagashima, K.V.; Igarashi, N.; Harada, J.; Nagashima, S.; Matsuura, K.; Shimada, K. Submitted to the EMBL Data Library, November 1999 #p.Description: Datermination of Nucleotide Sequences of Rubrivivax gelatinosus Photosynt A;Reference number: Z25270 #s.Accession: T50904 #s.Access
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:AE004228; GB:AE003552; NID:g9655997; PIDN:AAF94657.1; GSPDB:GN001
A;Experimental source: serogroup O1; strain N16961; biotype El Tor
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sun/nucleolar protein family protein VC1502 [imported] - Vibrio cholerae (strain N16961 C; Species: Vibrio cholerae (2; Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RiHeidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J. chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, I. R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         :Gene: bchH
;Superfamily: Rhodobacter capsulatus magnesium-protoporphyrin O-methyltransferase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein YOR253w - yeast (Saccharomyces cerevisiae) N;Alternate names: hypothetical protein 05315 C;Species: Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indela
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Pred. No. 5;
6; Mismatches 12;
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                                                    51.6%; Pred. No. 1.5; tive 2; Mismatches
                                                                                                                                                             4 HQHSMEIRTPDINPAWY----AGRGIRPVGR 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGR 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Experimental source: strain IL144 C;Genetics:
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Best Local Similarity 36.73
Matches 11; Conservative
                                                    Best Local Similarity 51.69
Matches 16; Conservative
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A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-503 < HBI>
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Best Local S
Matches 11
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K., Lim
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R;Xiong, J.; Inoue, K.; Bauer, C.B.
R;Xiong, J.; Inoue, Sci. U.S.A. 95, 14851-14856, 1998
A;Title: Tracking molecular evolution of photosynthesis by characterization of a major | A;Reference number: Z21036; MUID:99061957; PMID:9843979
                                                                                                                            Nypothetical protein ugpB [imported] - Agrobacterium tumefaciens (atrain C58, Dupont) p
                                                                                                                                                                                                                  C;Accession: AH3166
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClel; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2322, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                conserved hypothetical protein PA2151 [imported] - Pseudomonas aeruginosa (strain PAO1)
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C;Superfamily: Rhodobacter capsulatus magnesium-protoporphyrin O-methyltransferase
C;Keywords: lyase
                                                                                                                                                                                                                                                                                                                                                                                                                 ster, B.W.
A,Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A,Reference number: AB2577; MUID:21608550; PMID:11743193
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C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: F81376
R;Stover, C.Y.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, J. Lory, S.; Olson, M.V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 probable magnesium chelatase (BC 4.99.1.-) chain H BchH - Heliobacillus mobilis C;Species: Heliobacillus mobilis C;Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 15-Sep-2000
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A;Experimental source: strain C58 (Dupont)
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                                                                                                                                                             C,Species: Agrobacterium tumefaciens
C,Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
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A;Molecule type: DNA
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Matches 10; Conservative
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Best Local Similarity
Matches 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                       transcription regulator, ROK family Atu2609 [imported] - Agrobacterium tumefaciens (stra CiSpecies: Agrobacterium tumefaciens CiSpecies: Agrobacterium tumefaciens CiSpecies: Agrobacterium tumefaciens CiSpecies: Agrobacterium tumefaciens 11-Jan-2002 #text_change 18-Nov-2002 [Accession: AH2896 Riwood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I Riwood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I Kryp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001 AiAuthors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Agrobacterium tumefaciens
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 18-Nov-2002
C;Accession: B97672
C;Accession: B97672
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum A;Reference number: A97359; MUID:21608551; PMID:11743194
A;Accession: B97672
A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58. A;Reference number: AB2577; MUID:21608550; PMID:11743193 A;Accession: AH2896
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A;Residudes: 1-308 «KUXA»
A;Cross-references: GB:AE008688; PIDN:AAL43590.1; PID:g17741107; GSPDB:GN00186
A;Experimental source: strain C58 (Dupont)
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A;Map position: circular chromosome
C;Superfamily: conserved hypothetical protein H10182; glucose kinase homology
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A;Map positIon: circular chromosome
C;Superfamily: conserved hypothetical protein H10182; glucose kinase homology
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                                                              Length 73;
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Best Local Similarity 50.0%; Pred. No. 6.9;
Matches 10; Conservative 2; Mismatches
                                                       Query Match 30.2%; Score 52; DB Best Local Similarity 47.6%; Pred. No. 1.5; Matches 10; Conservative 3; Mismatches
                                                                                                                                                                                                                         23 AHTHRDEVRSACISVRWLAGR 43
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A; Map position: linear chromosome
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A; Status: nucleic acid sequence not shown; translation not shown
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A; Residues: 1-798 <JEF>
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R; Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; Ju, D. B.; Spadafora, R.; Vicaine, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N. Ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N. J. Bacteriol. 179, 7135-7155, 1997
A; Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct A; Reference number: A69000; MUID:98037514; PMID:9371463
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C;Species: Methanobacterium thermoautotrophicum
C;Date: 29-Jan_1999 #sequence_revision 29-Jan-1999 #text_change 23-Jul-1999
                               A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathd
A;Reference number: A82950; MUID:20437337; PMID:10984043
                                                                                    A;Accession: F83376
A;Status: preliminary
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-664 <STO>
A;Cross-references: GB:AE004642; GB:AE004091; NID:g9948163; PIDN:AAG05539.1; GSPDB:GN001
C;Genetics:
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A.Molecule type: DMA
A.Molecule type: DMA
A.Redidues: 1-294 «MI2>
A.Cross-references: EMBL:Z68115; PIDN:CAA92169.1; GSPDB:GN00028; CESP:F19H6.1
A.Experimental source: clone F19H6
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A;Molecule type: DNA
A;Residues: 1-294 <WIL>
A;Cross-teferences: EMBL:Z50873; PIDN:CAA90762.1; GSPDB:GN00028; CESP:F19H6.1
A;Experimental source: clone F17E5
R;McMurray, A.
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #squence_revision 15-Oct-1999 #text_change 17-Mar-2000
C;Accession: T21075; T21124
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A;Introns: 55/3; 85/2; 113/3; 150/1; 192/3; 266/2
C;Superfamily: kinase-related transforming protein; protein kinase homology
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Best Local Similarity 55.6%; Pred. No. 19;
Matches 10; Conservative 2; Mismatches
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A;Reference number: Z19368
A;Accession: T21075
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476 UNTPDINP-WFLQRSGRP 492
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406, 959-964, 2000
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Gene: CESP:F19H6.1
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A Molecule type: DNA
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C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Bate: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 05-Nov-1999
C;Accession: 511210
R;Jeffers, M.; Paciucci, R.; Pellicer, A.
Nucleic Acids Res. 18, 4891-4899, 1990
A;Title: Characterization of unr; a gene closely linked to N-ras.
A;Reference number: S11210; MUID:90370473; PMID:2204029
A;Accession: S11210
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0; Mismatches
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Pred. No. 27;
5; Mismatches
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Best Local Similarity 43.5%;
Matches 10; Conservative
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Best Local Similarity 69.2%;
Matches 9, Conservative
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rattus norv
homo sapien
bos taurus
homo sapien
corynebacte
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                                                                                                                                                                       December 3, 2003, 19:01:34; Search time 6.25 Seconds (without alignments) 233.252 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Description
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P91277
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P94972
Q9Jm52
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Q9Mp73
Q58172
Q58mp73
Q57996
Q9Fp39
Q57996
Q9Fp39
Q
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                            172
1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             127863 seqs, 47026705 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUMMARIES
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PRRP ATT
PRRP HUMAN
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EXTL CORGU
UNRA HILIGO
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NERS EXTL
TREPA
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                   OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Match Length DB
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Database :
                                                                                                                                                                                                                                                                                                                                                          Sequence:
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4 66 26.7 943 1 UVRA_BARIN P44410 haemophilus 6 45.5 26.5 273 1 TRAD_BROUN P050309 acceptabilis 6 45.5 26.5 273 1 TRAD_BROUN P050309 acceptabilis 6 45.5 26.5 273 1 TRAD_BROUN P050309 acceptable 6 45.5 26.5 274 1 TRAD_BROUN P050309 acceptable 6 45.5 26.2 377 1 TRAD_BROUN P050309 acceptable 6 45.5 26.2 377 1 TRAD_BROUN P050309 acceptable 7 TRAD_BROUN P05030 accept	## 46 26.7 943 1 35 46 26.7 943 1 36 45.5 26.5 272 1 38 45.5 26.5 374 1 38 45.5 26.5 374 1 38 45.5 26.5 411 1 45 26.2 418 44 48 48 44 45 26.2 418 44 48 48 44 48 48 44 48 48 44 48 48 44 48 48 44 48 48 44 4
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                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (ISOFORM 2).
STRAIN-Sprague-Dawley; TISSUE-Hypothalamus;
Anderson S.T., Kokay I.C., Lang T., Grattan D.R., Curlewis J.D.;
Quantitation of prolactin-releasing peptide (FrRP) mRNA expression in specific brain regions during the rat oestrous cycle and in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TPDINPAWYTGRGIRPVGRFGRRRATPRDVTGLGQLSCLPL
DGRTKPSQRG -> SECLTYGKQPLTSFHPFTSQMPP (in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Regul. Pept. 83:1-10(1999).
-!- FUNCTION: Stimulates prolactin (PRL) release and regulates the expression of prolactin through its receptor GPR10. May stimulate lactotrophs directly to secrete PRL.
                                                                                                                                            Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=99426652; PubMed=10498338;
Fujii R., Fukusumi S., Hosoya M., Kawamata Y., Habata Y., Hinuma S.
Sekiguchi M., Kitada C., Kurokawa T., Nishimura O., Onda H.,
                                                                                                                                                                                                                                              Hinuma S., Habata Y., Fujii R., Kawamata Y., Hosoya M., Pukusumi S. Kitada C., Masuo Y., Asano T., Matsumoto H., Sekiguchi M., Kurokawa T., Nishimura O., Onda H., Fujino M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sumino Y., Fujino M.; "Tissue distribution of prolactin-releasing peptide (PrRP) and its
                        PRRP_RAT STANDARD; PRI; 83 AA.
P81278; Q8K3Y0;
30-MAY-2000 (Rel. 39, Lest sequence update)
30-MAY-2000 (Rel. 34) Last annotation update)
28-FRB-2003 (Rel. 41, Last annotation update)
Prolactin-releasing peptide precursor (PrRP) (Prolactin-releasing hormone) (Contains: Prolactin-releasing peptide PrRP31; Prolactin-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IsoId=P81278-2; Sequence=VSP_004370;
TISSUE SPECIFICITY: Widely expressed, with highest levels in
medulla oblongata and hypothalamus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AMIDATION (G-53 PROVIDE AMIDE GROUP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROLACTIN-RELEASING PEPTIDE PRRP31.
PROLACTIN-RELEASING PEPTIDE PRRP20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR: JC7607; JC7607.

Hormone, Amidation; Signal; Cleavage on pair of basic residues; Alternative splicing.

Strenal.

1 21 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Name=1;
IsoId=P81278-1; Sequence=Displayed;
                                                                                                                                                                                                                                    MEDLINE=98268781; PubMed=9607765;
                                                                                                                                                                                                            SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AB015418; BAA29026.1; -. EMBL; AF521930; AAM82154.1; -.
                                                                                                                   releasing peptide PrRP20]
                                                                                                                                                                                                                                                                                                      Nature 393:272-276(1998)
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                                                                                                                                                                                 NCBI_TaxID=10116;
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33
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PEPTIDE
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RESULT 2
PRRP_RAT
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the RWBL outstation the Buropean Bloinformatics Institute. There are no restrictions on its was by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.lsb-sib.ch/announce/or send an email to license@sib.ch).
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-1- FUNCTION: Stimulates prolactin (FRL) release and regulates the expression of prolactin through its receptor GPR10. May stimulate lactotrophs directly to secrete FRL.

-1- TISSUR SPECIFICITY: MEDULLA OBLONGATA AND HYPOTHALAMUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Hinuma S., Habata Y., Fujii R., Kawamata Y., Hosoya M., Fukusumi S.,
Kitada C., Masuo Y., Asano T., Matsumoto H., Sekiguchi M.,
Kurokawa T., Nishimura O., Onda H., Fujino M.;
Ha prolactin-releasing peptide in the brain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=99426652; PubMed=10498338; Fujil R., Fukusumi S., Hosoya M., Kawamata Y., Habata Y., Hinuma S., Sekiguchi M., Kitada C., Kurokawa T., Nishimura O., Onda H., Sumino Y., Pujino M.; Fujino M.; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2003 (Rel. 41, Last annotation update)
Prolactin-releasing peptide precursor (PrRP) (Prolactin-releasing hormone) (Contains: Prolactin-releasing peptide PrRP31; Prolactin-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AMIDATION (G-54 PROVIDE AMIDE GROUP).
229A2F3F50CF981B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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PROLACTIN-RELEASING PEPTIDE PRRP20.
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Pred. No. 1.9e-16;
1; Mismatches 2; Indels
                                                                                                                                                                    Length 83;
                                                                                                                                                                                                                                           Indels
isoform 2).
/FTId=VSP 004370.
DOC75A264EEE4F29 CRC64;
                                                                                                                                                   Score 163; DB 1; L. Pred. No. 3.3e-17; ... Mismatches 2;
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                                                                                                                                                                                                                                                                                                                               1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31
                                                                                                                                                                                                     Pred. No. 3.36
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                         GO; GO:0005180; F:peptide hormone; TAS
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illarity 90.3%;
Conservative 1
                                                                                                                                                                    94.8%;
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Conservative
                                                                                    83 AA; 9215 MW;
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9639 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sapiens (Human)
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                                                                                                                                                                                             Local Similarity
ses 29; Conserv
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Matches 28; Conserv
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Matches
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195 RARPHSLMIYSDDLGATWHHGRLIKPM 221
2 RAHQHSMEIRTPDINPAWYAGRGIRPV
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                                                                                                                                  28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Sialidase 3 (Rel. 41, Membrane sialidase)
(N-acetyl-alpha-neuraminidase 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                       glycoconjugates.

GrantyTic Activity: Hydrolysis of alpha-(2->8)-, alpha-(2->6)-, alpha-(2->8)-glycosidic linkages of terminal sialic residues in oligosaccharides, glycoproteins, glycolipids, colominic acid and synthetic substrates.

SINGELLUIAR LOCATION: Membrane-associated (By similarity).

TISSUE SPECIFICITY: Expressed in brain.

SIMILARITY: BELONGS TO FAMILY 33 OF GLYCOSYL HYDROLAGES.
SIMILARITY: Contains 3 BNR repeats.
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                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                         Miyagi T., Wada T., Iwamatsu A., Hata K., Yoshikawa Y., Tokuyama
                                                                                                                                                                                                                                                                                                                                                                    FROM N.A., PARTIAL SEQUENCE, AND CHARACTERIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35.5%; Score 61; DB 1; Length 428; 40.7%; Pred. No. 0.2;
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By similarity.
Potential.
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                                      53
                                                                                                          428 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Interpro; IPR002860; GH_BNR.
Pfam; PF02012; BNR; 3.
Hydrolase; Glycosidase; Membrane; Repeat.
                          Potential.
Potential.
Potential.
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BNR 2.
BNR 3.
                                                                                                                                                                                                                                                                                                                              MEDLINE=99143165; PubMed=9988745;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           47916 MW;
                                                                                                                                                                                                                   taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          128 AA;
                                                                                                                                                                                                                                                                        NCBI_TaxID=9913;
                                                                                                          NER3 BOVIN
097859;
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REPEAT
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                                                                                              (Ganglioside sialidase)
                                                                                                                                                                                                                                                                    TISSUE-Brain;
MEDLINE-99335353; PubMed=10405317;
Wada T., Yoshikawa Y., Tokuyama S., Kuwabara M., Akita H., Miyagi T.;
"Cloning, expression, and chromosomal mapping of a human ganglioside
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTARLYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-, alpha-(2->6)-, alpha-(2->8)-glycosidic linkages of terminal stalic residues in oligosaccharides, glycoproteins, glycolipids, colominic acid and synthetic substrates.

--- SUBCENLIARA LOCATION: Membrane-associated
---- SUBCENLIARA LOCATION: Membrane-associated, adrenal gland and thymus, followed by pancreas, liver, heart and adrenal gland and thymus, followed by pancreas, liver, heart and thymus "Weakly expressed in kidney, placenta, brain and lung.
---- HISCELLANEOUS: Optimum pH is 3.8.
---- SIMILARITY: CONTAINS 3 BNR repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Monti B., Bassi M.T., Papini N., Riboni M., Manzoni M., Venerando B., Croci G., Preti A., Ballabio A., Tettamanti G., Borsani G., **Identification and expression of NBU3, a novel human sialidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -i- FUNCTION: Plays a role in modulating the ganglioside content of the lipid bilayer at the level of membrane-bound sialyl
                                                                                                                                                                        Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalla; Butheria; Primates; Catarrhini; Hominidae; Homo.
NER3 HUMAN STANDARD; PRT; 428 AA.
Q9UQ49; Q9NQR1;
28-FRB-2003 (Rel. 41, Created)
28-FRB-2003 (Rel. 41, Last sequence update)
28-FRB-2003 (Rel. 41, Last annotation update)
Sialidase 3 (RC 3.2.1.18) (Membrane sialidase)
                                                                                                                                                                                                                                                                                                                                                                lochem. Blophys. Res. Commun. 261:21-27(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GO; GO: 0005689; C: integral to plasma membrane, GO; GO: 0005689; C: integral to plasma membrane, GO; GO: 0006689; P: ganglioside catabolism; TAS. InterPro; IPR002866; GH_BNR. PF02012; BNR; 3. PROTOLABE; GlyCosldane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FRIP MOTIF.
By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               associated to the plasma membrane."; Biochem. J. 349:343-351(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BNR 1.
BNR 2.
BNR 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AB008185; BAA82611.1; -.
EMBL; Y18563; CAB96131.1; ALT_INIT.
                                                                                                                 (N-acetyl-alpha-neuraminidase 3)
                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
TISSUE=Skeletal muscle;
PubMed=10861246;
                                                                                                                                                      Homo sapiens (Human)
                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                             NCBI_TaxID=9606;
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Indels

Pred. No. 0.2; 6; Mismatches

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Local Similarity les 11; Conserv

Best Loca Matches

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Similarity
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SEQUENCE FROM N.A.
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                                               15-SEP-2003 (15-SEP-2003 (15-SEP-2003 (
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                            EX7L COREP
Q8FQF1;
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                     EX7L_COREP
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6
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28-FEB-2003 (Rel. 41, Last annotation update)
Probable exodeoxyribonuclease VII large subunit (BC 3.1.11.6)
                                                                                                                                                                                                                                                                                             Corynebacterium glutamicum (Brevibacterium flavum).
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30.2%; Score 52; DB 1; Length 417; 57.1%; Pred. No. 4.1; ive 1; Mismatches 0; Indels
                                                                                                  Score 56; DB 1; Length 428;
Pred. No. 1.1;
                                                                                                                      11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam, PF02601; Exonuc_VII_L; 1.
TIGRTAMS; TIGR00237; ExeA; 1.
Hydrolase; Nuclease; Exonuclease; Complete proteome.
SEQUENCE 417 AA; 45582 MW; B32CD9286C173C34 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAY LOCATION: Cytoplasmic (By similarity). SIMCELLULAY LOCATION: Cytoplasmic (By similarity). SIMILARITY: BELONGS TO THE XSEA FAMILY.
                                                                              35D1DD9359A78C98 CRC64;
                   Potential.
Potential.
Potential.
By similarity.
Potential.
                                                                                                                                                                                                                417 AA
                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
Nakagawa S.;
                                                                                                                      6; Mismatches
                                                                                                                                                      2 RAHQHSMEIRTPDINPAWYAGRGIRPV 28
                                                                    Potential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HAMAP; MF 00378; -; 1.
InterPro; IPR003753; Exonuc VII L.
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|PAFYAGRGIFSLWVIDIRPVG 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17 PAWYAGRG-----IRPVG 29
                                                                                                                                                                                                                                                                         (Exonuclease VII large subunit).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AP005277; BAB98418.1; -.
                                                                                                                                                                                                                                    (Rel. 41, Created)
                                                                               48252 MW;
                                                                                                  32.6%;
37.0%;
                                                                                             Ouery Match
Best Local Similarity 37.00
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12; Conservative
                                                                                                                                                                                                                STANDARD;
                                                                   387
428 AA;
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                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=1718;
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ID EX7L C
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                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus (Rat).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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                                                 IS-SEP-2003 (Rel. 42, Created)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Probable exodeoxyribonuclease VII large subunit (EC 3.1.11.6)
                                                                                                                                                                                                                             Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales, Corynebacterineae, Corynebacteriaceae, Corynebacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30.2%; Score 52; DB 1; Length 447; 57.1%; Pred. No. 4.4; 0; Indels :ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HAMAP; MP 00378; -; 1.

InterPro; IPR003753; Exonuc_VII_L.
Pfam; PP02601; Exonuc_VII_L; 1.

TIGRAMS; TIGR00237; xseA; 1.

Hydrolase; Nuclease; Exonuclease; Complete proteome.
SEQUENCE 447 AA; 49051 MW; FDBDF6A768E742C1 CRC64;
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-!- SUBCELLIAY.
-!- SUBCELLIAY.
-!- SIMILARITY: BELONGS TO THE XSEA FAMILY.
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01-NOV-1990 (Rel. 16, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
447 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PAWYAGRG-----IRPVG 29
                                                                                                                                                  (Exonuclease VII large subunit).
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                                                                                                                                                                                                                Corynebacterium efficiens.
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STANDARD;
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UvrABC system protein A (UvrA protein) (Excinuclease ABC subunit A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                Jeffers M., Paciucci R., Pellicer A.;
"Characterization of unr; a gene closely linked to N-ras.";
Nucleic Acids Res. 18.4891-4899 (1990).
--- FUNCTION: RNA-BINDING PROTEIN (BY SIMILARITY).
--- SUBCELLULAR LOCATION: Cytoplaemic.
--- SIMILARITY: BELONGS TO THE COLD-SHOCK DOMAIN (CSD) FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Archaea, Buryarchaeota, Methanobacteria, Methanobacteriales,
Methanobacteriaceae, Methanothermobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29.7%; Score 51; DB 1; Length 798;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CSD 1.
CSD 2 (INCOMPLETE).
CSD 3.
CSD 5.
CSD 6.
CSD 6.
CSD 7.
CSD 7.
CSD 7.
CSD 9.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL, X52311; CAA36549.1; -.
PIR; S11210; S11210.
HSSP, P15277; IMC.
Interer: IRR002059; Cold_shock.
Pfam; PP00313; CSD; 7.
ProDom; PD000621; Cold_shock; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=Delta H;
MEDLINE=98037514; Pubmed=9371463;
                            MEDLINE=90370473; PubMed=2204029;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART; SM00357; CSP; 5.
PROSITE; PS00352; COLD_SHOCK; 4.
RNA-binding; Repeat.
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(Rel. 39, Last seqn
(Rel. 41, Last anno
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nes 10; Conservative
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SEQUENCE FROM N.A.
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TISSUE=Testis;
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    (By similarity).
    -1- SUBGUNIT: Forms a heterotetramer with uvrB during the search for lesions (By similarity).
    -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
    -1- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. UVRA SUBPAMILY.

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                         processing of DNA lesions. UvrA is an Arrase and a DNA-binding protein. A damage recognition complex composed of 2 uvrA and 2 uvrB subunits scans DNA for abnormalities. When the presence of lesion has been verified by uvrB, the uvrA molecules dissociate
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Pasteurellaceae, Pasteurella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 51; DB 1; Length 962; Pred. No. 14; 0; Mismatches 5; Indels
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962 AA; 108395 MW; 2COEF7FC41CCD060 CRC64;
FUNCTION: The UvrABC repair system catalyzes the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      703 ŘÍPRSNPÁTYTGVFTHIRELFAQTPEARKRGYRP-GRF 739
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ATP (POTENTIAL).
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16-007-2001 (Rel. 40, Last sequence update)
16-007-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             288 AA.
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HAWAP, MP 00205; -; 1.
Interpro; IPR00359; 3AA ATPase.
Interpro; IPR003493; ABC_transporter.
Interpro; IPR004602; UvrĀ.
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MEDLINE=21145866; PubMed=11248100;
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39.5%;
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Best Local Similarity 39.5
Matches 15, Conservative
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SEQUENCE
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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SUBUNIT: Forms a heterotetramer with uvrB during the search for lesions (By similarity).
SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. UVRA SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=21082930; PubMed=11214968;
Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S., Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.; "Complete genome structure of the nitrogen-fixing symbiotic bacterium
                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mesorhizobium loti.";

DNA Res. 7:331-338(2000).

-!- FUNCTION: The UVLABC repair system catalyzes the recognition and processing of DNA lesions. UvrA is an ATPase and a DNA-binding processing of DNA lesions. On complex composed of 2 uvrA and 2 uvrB subunits scans DNA for abnormalities. When the presence of lesion has been verified by uvrB, the uvrA molecules dissociate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
UVRABC system protein A (UVRA protein) (Excinuclease ABC subunit A).
                                                                                                                                                                                                                                                                         ö
                                                                                                                  InterPro; IPR005581; Fructosamin kin.
Pfam; PP03881; Fructosamin kin, I.
Hypothetical protein; Transferase; Kinase; Complete proteome.
SEQUENCE 288 AA; 33778 MW; P4D2F6C26014D940 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Phyllobacteriaceae; Mesorhizobium.
VOBI_TaxID=381;
                                                                                                                                                                                                                            Query Match
29.1%; Score 50; DB 1; Length 289;
Best Local Similarity 37.5%; Pred. No. 5.4;
Matches 9; Conservative 6; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                               973 A.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HAMAP; MF_00205; -; 1.
InterPro; IPR003439; ABC_transporter.
InterPro; IPR004602; UvrA.
                                                                                                                                                                                                                                                                                                                5 QHSMEIRTPDINPAWYAGRGIRPV 28
                                                                                                                                                                                                                                                                                                                                        20 KHKEKIHTGEMHEAWIIDDGIQPV 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rhizobium loti (Mesorhizobium loti).
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                                                                                                 EMBL; AE006094; AAK02671.1; -.
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Q98M36;
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UVRA_RHILO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          *Regulation of divergent transcription from the uvrA-ssb promoters in Sinorhizobium mellioti.";

*Riorhizobium mellioti.";

*Mol. Gen. Genet. 262:121-130(1999).

-I- FUNCTION: The UvrABC repair system catalyzes the recognition and processing of DNA lesions. UvrA is an ATPase and a DNA-binding protein. A damage recognition complex composed of 2 uvrA and 2 uvrB subunits scans DNA for abnormalities. When the presence of a lesion has been verified by uvrB, the uvrA molecules dissociate
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--- SUBUNIT: Forms a heterotetramer with uvrB during the search for lesions (By similarity).
--- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
--- SUBCELLULAR LOCATION: THE ABC TRANSPORTER FAMILY. UVRA SUBFAMILY.
SOS response; Excision nuclease; DNA repair; DNA recombination; DNA excision; ATP-binding; DNA-binding; Repeat; Zinc; Metal-binding; Zinc-finger; Complete proteome.
                                                                                                                                                                                                        Gaps
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30-MAY-2000 (Rel. 39, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
VOYARC system protein A (UVAX protein) (Excinuclease ABC subunit A).
UVRA OR R01557 OR SWC01235.
Rhizobium melilori (Sinorhizobium melilori).
Bacteria, Proteobacteria, Alphaproteobacteria; Rhizobiales;
Rhizobiacese; Sinorhizobium/Ensifer group; Sinorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J., Bolstard P., Becker A., Boutry M., Cadieu B., Dreano S., Gloux S., Godrie T., Goffeau A., Kahn D., Kish B., Lelaure V., Masuy D., Pohl T., Portetelle D., Puehler A., Purnelle B., Ramsperger U., Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F., "Analysis of the chromosome sequence of the legume symbiont
                                                                                                                                                                                                        18;
                                                                                                                                                              29.1%; Score 50; DB 1; Length 973; 39.5%; Pred. No. 19;
                                                                                                                                                                                                      3; Indels
                                                                                                   761 787 C4-TYPB.
973 AA; 107358 MW; 767D7D2DC8220057 CRC64;
                                                                                                                                                                                                                                                                                      RIPRSNPATYTGAFIPIRDWFAGLPEAKARGYOP-GRF 752
                                                                                                                                                                                                                                              11 RIPDINPA-----WYAG-----RGIRPVGRF 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sinorhizobium meliloti strain 1021.";
Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
                                                           ATP (POTENTIAL)
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                                                                                (POTENTIAL)
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EMBL; AF125162; AAP03210.1; -.
HAMAB; MF_00205; -; 1.
InterPro; IPR003439; ABC_transporter.
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                                                                                                                                                                                                    15; Conservative
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Best Local Similarity
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P56899;
                                                           NP_BIND
NP_BIND
ZN_FING
SEQUENCE
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UVRA_RHIME
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Matches
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EMBL; D90916; BAA18726.1; ALT INIT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -i- CATALYTIC ACTIVITY: 6-phospho-D-glucono-1,5-lactone + H(2)0 = 6-phospho-D-gluconate.
-i- PATHWAY: Pentose phosphate pathway; second step.
-i- SIMILARITY: BELONGS TO THE GLUCOSAMINE/GALACTOSAMINE-6-PHOSPHATE ISOMERASE FAMILY. 6-PHOSPHOGLUCONOLACTONASE SUBFAMILY.
                             ProDom; PD000006; ABC transporter; 1.

TIGRFAMS; TIGR00630; uvra; 1.

PROSITE; PS00211; ABC TRANSPORTER 1; 2.

SOS TESPORES; ES5083; ABC TRANSPORTER 2; 1.

SOS TESPORES; ES5083; ABC TRANSPORTER 2; 1.

SOS TESPORES; ES5080; ATP-binding; DNA-binding; Repeat; Zinc; Metal-binding; Zinc-finger; Complete proteome.

NP BIND 62 669 ATP (POTENTIAL).

NP BIND 62 669 ATP (POTENTIAL).

ZN_FING 761 787 C4-TYPE.
                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=97061201; PubMed=8905231; Kannaka A., Asamizu E., Nakamura Y., Kannako T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y., Kannako T., Sato S., Kotani H., Tanaka A., Sasamoto S., Kimura T., Hosouchi T., Mateuno A., Muraki A., Nakazaki N., Naruo K., Okumura S., Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M., Tabata S., Siguence analysis of the genome of the unicellular cyanobacterium Symechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-97443974; PubMed-9298645;
Sazuka T., Ohara O.;
"Towards a proteome project of cyanobacterium Synechocystis sp.
strain PCC6803: linking 130 protein spots with their respective
                                                                                                                                                                                                                                                                                                                  3; Indels 18;
                                                                                                                                                                                                                                                                            Score 50; DB 1; Length 973;
Pred. No. 19;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Electrophoresis 18:1252-1258(1997).
-!- FUNCTION: HYDROLYSIS OF 6-PHOSPHOGLUCONOLACTONE TO 6-PHOSPHOGLUCONATE.
                                                                                                                                                                       662 669 ATP (POTENTIAL).
761 787 C4-TYPE.
19 19 G -> A (IN REF. 2).
67 67 F -> S (IN REF. 2).
973 AA; 107191 MW; 3E1A8B14527A47FE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Cyanobacteria; Chroococcales; Synechocystis
                                                                                                                                                                                                                                                                                                                                                                                     716 RIPRSNPATYTGAFIPIRDWPAGLPBAKARGYOP-GRF 752
                                                                                                                                                                                                                                                                                                                                                     11 RIPDINPA-----WYAG-----RGIRPVGRF 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1997 (Rel. 35, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) 6-phosphogluconolactonase (EC 3.1.1.31) (6PGL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               239 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1997 (Rel. 35, Created)
                                                                                                                                                                                                                                                                               29.1%;
                    tran; 2.
InterPro; IPR004602; UvrA.
                                                                                                                                                                                                                                                                                                                15; Conservative
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                                                                                                                                                                                                                                                                                                Local Similarity
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                                                                                                                                                                                                          CONFLICT
                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                              6PGL_SYNY3
                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 13
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                                                                                                                                                                                        ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'Complete sequence analysis of the genome of the bacterium Mycoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hilbert H., Himmelreich R., Plagens H., Herrmann R.; Requence analysis of 56 kb from the genome of the bacterium Mycoplasma pneumoniae comprising the dnaA region, the atp operon and cluster of ribosomal protein genes "; Nucleic Acids Res. 24:628-639(1996).
                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IDENTIFICATION BY MASS SPECTROMETRY.
STRAIN=AFCC 29342 / M129;
MEDLINE=21088919; PubMed=11271496;
Regula J.T., Ueberle B., Boguth G., Goerg A., Schnoelzer M.,
Hermann R., Frank R.;
"Towards a two-dimensional proceome map of Mycoplasma pneumoniae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Electrophoresis 21:3765-3780(2000).
-I- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-I- SIMILARITY: SOMB, TO MG064.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mycoplasma pneumoniae.
Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
                                                                                                                                                                                      ä
                                                                                                                                               28.2%; Score 48.5; DB 1; Length 239; 42.3%; Pred. No. 7.5; Live 5; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Himmelreich R., Hilbert H., Plagens H., Pirkl B., Li B.-C.,
                                                                                                                                                                                    9; Indels
InterPro; IPR006148; Gluc_gal_isom.
InterPro; IRR00590; Phosphogluconiac.
Pffam, PP01182; Glucosamine_iso; 1.
TIGRPAMs; TIGR01198; pgl; 1.
Hydrolase; Complete proteome.
0 0 0
SRQUENCE 239 AA; 26351 MW; 9C64A0A342325917 CRC64;
                                                                                                                                                                                                                                                                                                                                                      Y468_MYCPN STANDARD; PRT; 1882 AA. P75.109, Q50.317; Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) PRTGB-2003 (Rel. 41, Last annotation update) MPMC684 OR MP158.
                                                                                                                                                                                                                                                S QHSM-RIRTPDINPAWYAGRGIRPVG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic Acids Res. 24:4420-4449(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 1-1848 FROM N.A.
STRAIN=ATCC 29342 / M129;
MEDLINE=96177562; PubMed=8604303;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE PROM N.A.
STRAIN=ATCC 29342 / M129;
MEDLINE=97105885; PubMed=8948633;
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PIR; S73484; S73484.
InterPro; IPR003838; DUF214.
Pfam; PP02687; FteX; 1.
Transmembrane; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AE000017; AAB95806.1; -. EMBL; U34816; AAC43650.1; -.
                                                                                                                                 NCBI TaxID=2104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pneumoniae.
                                                                                                                                                                                                                                                                                                                     RESULT 14
Y468 MYCPN
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                                                                                                                                                                                                                                                                                                                                                                                                              Plasmid 60-mba cryptic.
Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Salmonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Salmonella typhimurium has two homologous but different umubC operons: cloning of a new umubC-like operon (samAB) present in a 60-megadalton cryptic plasmid of S. typhimurium."; Dacteriol. 173:1051-1063(1991).
-!- FUNCTION: INVOLVED IN UV PROTECTION AND MUTATION.
-!- SIMILARITY: BELONGS TO THE DNA POLYMERASE TYPE-Y FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                   DB 1; Length 1882;
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50.0%; Pred. No. 16;
ive 1; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=LT2;
MEDLINE=91123176; PubMed=1991707;
Nohmi T., Hakura A., Nakai Y., Watanabe M., Murayama S.Y.,
Sofuni T.;
                                                                                                                                                                              12; Indels
                                                                                                           POTENTIAL.
MW; 03CFA4D99A7120ED CRC64;
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                                                                                                                                                                                                                         01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                  Score 48.5; DB; Pred. No. 64; 6; Mismatches
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                         POTENTIAL.
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                                                                                                                                                                                                                                                                                                     PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HAMAP; MF_01113; atypical; 1.
InterPro; IPR001126; UMUC_like.
Pfam; PP00817; IMS; 1.
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                                                                                                                                                             Local Similarity 32.3%;
nes 10; Conservative
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Best Local Similarity 50.0°
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                   Salmonella typhimurium.
                            1057
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1759 177
1807 182
1828 184
1851 187
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P23832;
TRANSMEM
SEQUENCE
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SAMB_SALTY
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Search completed: December 3, 2003, 19:12:02
Job time : 7.25 secs
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Q8ukp2 agrobacteri Q8cbt2 mus musculu Q8cpt2 mus musculu Q8c720 mus musculu Q8c720 mus musculu Q9zge5 heliobacill Q9zge5 heliobacill Q9zge5 heliobacill Q9sgr0 xanthomonas Q1530 caenorhabdi Q81474 burkholderi Q95664 homo sapien Q85664 homo sapien Q85664 homo sapien Q85664 homo sapien Q8721 mus musculu Q2142 methanobact Q27142 methanobact Q9vr73 drosophila Q81z1 mus musculu Q81z1 mus musculu

QBUKP2 QBCDT2 QBC72 QBC72 QBBT77 Q92GES Q94F29 Q911W4 Q87F80 Q911W4 Q86SD4 Q96SD4 Q96S

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01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                         830525
                    GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                172
1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31
                                                                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                 830525 seqs, 258052604 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                protein search, using sw model
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Q6V687
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and is derived by analysis of
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Maximum DB seq length: 200000000
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Match Length
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Perfect score:
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ALIGNMENTS

Q8R3R1 Q8JZN2 Q91W50 Q8T4U2 Q8TTS7 Q8S7E3 Q8S7E3

!	PRELIMINARY; PRT; 98 AA.			Preproprolactin-releasing peptide.	Ovis aries (Sheep).		Mammalla; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;	Japrinae; Ovis.	こうずんの	A N MOR	Curlewis J.D., Kusters D.H.L., Barclay J.L., Anderson S.T.;	1-releasing peptide (PrRP) in the ewe: cDNA clos	distribution and effects on prolactin secretion in vitro and	Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.	SMBL; AF450453; AAL4/1/8:1;	98 AA; 10513 MW; 2A53331ED62CAABS CRC64;	100.0%; Score 172; DB 6; Length 98; milarity 100.0%; Pred. No. 9.2e-17; Conservative 0; Mismatches 0; Indels	SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31			PRELIMINARY: PRT: 117 AA.	, , , ,
ğ	ID Q8WN12 AC O8WN12;		DT 01-MAR-2002	DB Prepropro	OS Ovis arie	_			OA NCBI_TAXID=9940; DN [1]	•					DK EMBL; AF4	Q SEQUENCE	Query Match Best Local Similarity Matches 31; Conserv	0,7	Db 23 (RESULT 2	09W624 TD 09W624	

Gaps

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SOCOCOSTATA

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Bukaryota, Metazoa, Chordata, Urochordata, Ascidiacea, Enterogona,
Phlebobranchia, Cionidae, Ciona.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        [1] SRQUENCE FROM N.A. SRQUENCE FROM N.A. SRQUENCE FROM N.A. KUNOSSAWA H., Inukai T., Inaba T., Goi K., Chang K.-S., Sinjyo' Rakestraw K.M., Naeve C.W., Look T.A.; Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

Imal K.S., Satch N., Satcu Y.;
I "Clona savignyl genes";
" "Clona savignyl genes";
" Submitted (MAR-201) to the EMBL/GenBank/DDBJ databases."
RMEL; AB057747; BAB68356.1;
" InterPro; IRR007087; Znf C2H2.
R Pfem; PF00096; Znf C2H2; 4.
R PROSITE; PS00028; ZINC FINGER C2H2.1; 3.
R PROSITE; PS00028; ZINC FINGER C2H2.2; 4.
Metal-binding; Zinc; Zinc finger.
D SEQUENCE 355 AA; 40876 MW; R58F5DEDDB12E8AC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 33.1%; Score 57; DB 5; Length 355; Best Local Similarity 40.0%; Pred. No. 7; Matches 12; Conservative 7; Mismatches 7; Indels
                                                                                                                                         Length 54;
                                  Lawlor 8.;
Submitted (BEP-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AL035608; CAB55682.1; -.
NON TER 54 54
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01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Sushi-repeat protein (Sushi-repeat containing protein)
                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                         Score 57; DB 4;
Pred. No. 0.98;
                                                                                                       SEQUENCE 54 AA; 6110 MW; E2F3C39F7B961A9F
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                                                                                                                                                                                                                                                                                                                                                                                    Created)
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56.2%;
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01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
01-MAR-2003 (TrEMBLrel. 23,
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CS-ZICRIA.
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                                                                                                                                                            Best Local Similarity
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SEQUENCE FROM N.A.
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                                                                                                                                           Query Match
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       Carassius auratus (Goldfish).

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Actinopterygili, Neopterygili, Teleosteli, Ostariophysi, Cypriniformes,
Cyprinidae, Carassius.

NCBI_TaxID=7957,
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Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=R5;

RDDINRE-20138142; PubMed=10671438;

Cheng Y.S., Brantner C.A., Taapin A., Collins M.L.P.;

Cheng Y.S., Brantner C.A., Taapin A., Collins M.L.P.;

"Role of the H protein in assembly of the photochemical reaction center and intracytoplasmic membrane in Rhodospirillum rubrum.";

J. Bacteriol. 1821200-1207(2000).

EMBL; AR202319; AAR37352.1;

EMBL; AR202319; AAR37352.1;

EMBL; AR202319; CobN/Mg_chltase.

Pfam; PF02514; cobN-Mg_chel; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria, Proteobacteria, Alphaproteobacteria, Rhodospirillales,
Rhodospirillaceae, Rhodospirillum.
NCBI_TaxID=1085;
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                                                                                                                                                                                                                                                                         Length 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 36.0%; Score 62; DB 2; Length 692; Best Local Similarity 40.6%; Pred. No. 2.7; Matches 13; Conservative 4; Mismatches 9; Indels
                                                                                                                                                                                                                                                                       Query Match 60.5%; Score 104; DB 13; Length 1 Best Local Similarity 57.7%; Pred. No. 4.8e-07; Matches 15; Conservative 8; Mismatches 3; Indels
                                                                                                                                       692 AA; 75453 MW; 96430AE93BF35680 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-2000 (TrEMBLrel. 13, Created)
WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DJ479J7.3 (Sushi-repeat protein (SRPUL)) (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
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                                                                                                                            SEQUENCE FROM N.A.
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MEDLINE=21595285; PubMed=11759840;
Kaneko T., Nakemura Y., Wolk C.P., Kuritz T., Sasamoto S.,
Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,
Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,
Yasuda M., Tabata S.;
                                                                                                        Complete genomic sequence of the filamentous nitrogen-fixing cyanobacterium Anabaena sp. strain PCC 7120.";
DNA Res. 8:205-213(2001).
BMBL; AP003586; BAB78052.1; -
InterPro; IPR004843; M-ppestrase.
Ffam; PR00449; Metallophos; I.
Hypothetical protein; Complete proteome.
SEQUENCE 303 AA; 34449 MW; 685700B2127E8987 CRC64;
                                                                                                                                                                                                                                                                     Best Local Similarity
Matches 16, Conserv
      SEQUENCE FROM N.A.
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duang C.-H., Chen H., Peng J., Chen Y., Cloning and characterization of the sushi-repeat containing protein (SRP) as a novel interaction partner of Rh type C glycoprotein
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Strausberg R.;
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
BMBL; BC020733, AAH20733.1;
InterPro; IPR00128; Cytcdirome_P450.
InterPro; IPR001310; Hyalin.
InterPro; IPR000436; Sushi_SCR_CCP.
Pfan; PP00494; HYR; 1.
Pfan; PP00494; HYR; 1.
Rean; PP00494; Bushi; 3.
SMART; SM00084; Bushi; 3.
SMART; SM00086; CYTCHOME_P450; 1.
SEQUENCE 465 AA; 52957 MW; 3D7229487DAlbBBD CRC64;
                                                                                                                                                                                                                                    33.1%; Score 57; DB 4; Length 465; S6.2%; Pred. No. 9.2; tive 1; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 57; DB 4; Length 465;
Pred. No. 9.2;
1; Mismatches 6; Indels
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Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
NCBL_TaxID=103690;
                                                          Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF060567; AAC15765.1; -...
EMBL; AF8393649; AAM73693.1; -...
InterPro; IPR001128; Cytochrome_P450.
InterPro; IPR001410; Hyalin.
InterPro; IPR003416; Sushi_SCR_CCP.
Pfam; PF00494; HYR; 1.
                                                                                                                                                                                     PROSITE; PS00086; CYTOCHROME P450; 1.
SEQUENCE 465 AA; 52971 MW; 4D752B187FF3EFB8 CRC64;
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01-MAR-2002 (TYEMBLrel. 20, Last sequence update)
01-MAR-2003 (TYEMBLrel. 23, Last annotation update)
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01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein All1686.
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Local Similarity 56.2%;
les 9; Conservative
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Homo sapiens (Human).
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                                                                                                    Gaps
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MEDLINE=20031519; PubMed=10563807;
Menin L., Yoshida M., Jaquinod M., Nagashima K.V., Matsuura K.,
Parot P., Vermeglio A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=IL144;
Nagashima K.V., Shimada K., Matsuura K.;
"Phylogenetic analysis of photosynthetic genes of Rhodocyclus gelatinosus: Possibility of horizontal gene transfer in purple
                                                                                                5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rhodocyclus gelatinosus (Rhodopseudomonas gelatinosa).
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Comamonadaceae; Rubrivivax.
                          DB 16; Length 303;
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                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDINE-94132007; PubMed-8300574; Nagashima K.V., Matsuura K., Ohyama S., Shimada K.; Primary structure and transcription of genes encodi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Mg protoporphyrin methyl transferase.
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32.8%; Sco. No. ', 51.6%; Pred. No. ', 2, Mismatches
                                                                                                                                                                                                                                           226 HEHSYB-RIRAIDGITYLICGAGAGNRPVGR 255
                                                                                                                                                                                                                                                                                                                                                                                                                                               1236 AA
                                                                                                                                                                     4 HQHSMEIRTPDINPAWY----AGRGIRPVGR 30
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                                                                                                16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PAC COCCOS REPRESENTATOR REPRE
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Jauniaux J.C., Poirey R.; "Sequencing analysis of a 36.8 kb fragment of yeast chromosome XV reveals 26 open reading frames including SBC63, CDC31, SUG2, GCD1, RBL2, PNT1, PAC1 and VPH1."; Yeast 131483-487(1997).
           Bukaryota; Fung1; Ascomycota; Saccharomycotina; Saccharomycetes;
Baccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBI TaxID=4932;
                                                                                                                                                          Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases
Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                               EMBL; Z75161; CAA99475.1; -.
SGD; S0005779; ARD2.
InterPro; IPR000185; CytC heme bind.
InterPro; IPR000182; GCN5acetyItransf.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam, PP00583; Acetyltransf; 1.
PROSITE; PS00190; CYTOCHROME C; 1.
SEQUENCE 176 AA; 19727 MW; 4F0
                                                                                                                                                                                                                            MEDLINE=97298311; PubMed=9153759;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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SEQUENCE 376 AA;
                                                                                                                                                                                                     SEQUENCE PROM N.A.
                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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Matches
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STRAINEEL TOR N16961 / Serotype Ol;

MEDLINE=20406833; PubMed=10952301;

MEDLINE=20406833; PubMed=10952301;

Meddelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,

Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,

Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,

Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,

McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,

Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,

Fraser C.M.;
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    potential cytochrome c8 in the photosynthetic bacterium
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                                                                                                                                                                                                     32.0%; Score 55; DB 2; Length 1236; 34.4%; Pred. No. 49; ive 6; Mismatches 9; Indels
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                                                                                                                                                             1236 AA; 134729 MW; 84051C045638520C CRC64;
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Last sequence update)
Last annotation update)
ORF YOR253W.
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Sun/nucleolar protein family protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12;
                                                                                                                                                                                                                                                                                                                               3 AHQHSMEIRTPDINPAWYAG-----RGIRPV 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                           503 A.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31.7%; Score 54.5; 36.7%; Pred. No. 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6; Mismatches
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                                                                 EMBL; AB034704; BAA94057.1; -.
InterPro; IPR03672; CobN/Mg_chltase.
Pfam; PP02514; cobN-Mg_chel; 1.
Transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TIGR; VC1502; ...
InterPro; IPR000051; SAM bind.
InterPro; IPR001678; Sun_Nop1/Nop2.
Pfam; PF01189; Nol1 Nop2 Sun; 1.
TIGRFAMB; TIGR00446; nop2p; 1.
PROSITE; PS01153; NOL1_NOP2_SUN; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                              Biochemistry 38:15238-15244(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AE004228; AAF94657.1; -.
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                                                                                                                                                                                                                                                      11; Conservative
    midpoint potential cytoch
Rubrivivax gelatinosus."
                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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                                                                                                                                                                                                       Query Match
Best Local Similarity
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                                                                                                                                                               SEQUENCE
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008689
ID 00868
AC 00868
DT 01-NC
DT 01-MC
DT 01-MG
DE Chrom
GN ARD2
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                                                                                                              3;
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                                            Query Match
31.1%; Score 53.5; DB 3; Length 176;
Best Local Similarity 31.2%; Pred. No. 11;
Matches 10; Conservative 5; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Genome sequence of the radioresistant bacterium Deinococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 376;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria, Deinococcus-Thermus, Deinococci, Deinococcales, Deinococcaceae, Deinococcus.
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4F09DC597A690BA0 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
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40.0%; Pred. No. 27;
tive 6; Mismatches 12.
                                                                                                                                                                                                       120 SECHQHNVFVYLPAVDDLTKQWFIAHGFEQVG 151
                                                                                                                                                                   1 SRAHQHSMEIRTP---DINPAWYAGRGIRPVG 29
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                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Adenine deaminase-related protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=20036896; PubMed=10567266;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         radiodurană Rl.";
Science 286:1571.1577(1999).
EMBL; AEVO1863; ARF12376.1; -
TIGR; DRAO268; -.
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01-JUN-2002 (
01-JUN-2002 (
01-JUN-2002 (
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Q8U515;
                                                                                                              RESULT 15
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Huang C.-H., Chen H., Peng J., Chen Y.;

"Cloning and characterization of the sushi-repeat containing protein (SRP) as a novel interaction partner of Rh type C glycoprotein (RhCG).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                   Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11100395C7RIK.
Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30.8%; Score 53; DB 11; Length 468; 53.3%; Pred. No. 34; 1; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF393640; AAM73691.1; --
MGD; MGI:1916042; 1110039C07Rik.
                                                                                                                                                                                                                                                                                                                                            Strausberg R., Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SM00032; CCP; 3.
PROSITE; PS00086; CYTOCHROME P450; 1.
SEQUENCE 467 AA; 53009 MW; BB4C01C7E6118BE0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100086; CYTOCHROME P450; 1.
468 AA; 53180 MW; 151A952070D040D4 CRC64;
                                                                                                              Last sequence update)
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Last annotation update)
                                               467 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 468 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IPR001128; Cytochrome P450.
IPR003410; Hyalin.
IPR000436; Sushi_SCR_CCP.
                                                                                         Created)
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                                            PRT;
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                                                                                  01-000-2002 (TrEMBLrel. 21, Crea
01-00N-2002 (TrEMBLrel. 21, Last
01-MAR-2003 (TrEMBLrel. 23, Last
Similar to sushi-repeat protein.
1110039C07RIK.
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PAVTPTWYAGSGYSP 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 53.33
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF02494; HYR; 1.
Pfam; PF00084; sushi; 3.
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                                            PRELIMINARY;
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Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                        NCBI_TaxID=10090;
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RESULT 13
Q8R054
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Q8K1F8
                                            DATOOCCOOR BEAR BRANK BR
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Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M., Goodner B., Hinkle G., Gattung S., Miller N., Halling C., Mullin L., Gurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L., Houmiel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F., Willam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B., Flansgan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G., Cielo C., Slater S., "Genome sequence of the plant pathogen and biotechnology agent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                               AGR_L_105.
AGR_LT_105.
AGrobacterium tumefaciens (strain C58 / ATCC 33970).
Bacteria: Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Rhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30.2%; Score 52; DB 16; Length 73; 47.6%; Pred. No. 6.9; tive 3; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Science 294:2323-2328(2001).
EMBL; AE008203; AAK88619.1; -.
SEQUENCE 73 AA; 8219 MW; 02A6F70FA651F2AB CRC64;
                                                                                                                                                                                                                                                                                             (TrEMBLrel. 21, Last sequence update) (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                          73 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Search completed: December 3, 2003, 19:14:01 Job time : 27.5 secs
                                                                                                                                                                                                                                                              (TrEMBLrel. 21, Created)
                                                                                                                                                                                                          PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23 AHTHRDEVRSACISVRWLAGR 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Agrobacterium tumefaciens C58."; Science 244.222-110.
13 PDINPAWYAGRGIRP 27
                                       20 PAVTPTWYAGSGYSP 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 47.6
Matches 10; Conservative
                                                                                                                                                                                                       PRELIMINARY;
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

December 3, 2003, 18:57:14 ; Search time 33.75 Seconds (without alignments) 145.793 Million cell updates/sec Run on:

US-09-868-885B-18 Title: Perfect score:

174 1 SRAHQHSMETRTPDINPAWYTGRGIRPVGRF 31 Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

1107863 Total number of hits satisfying chosen parameters:

1107863 seqs, 158726573 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT:*/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2003.DAT:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Rat type G protein	Rat type ligand po	Rat 19P2 ligand.	Murine pituitary-d	Murine pituitary-d	Rat oxytocin secre	Rat prolactin-rele	19P2 ligand peptid	Rat CRH releasing
SUMMERTES	QI	AAW31384	AAW97233	AAW87614	AAW95173	AAW95174	AAB10355	AAY87504	AAY49292	AAG62524
	рв	18	20	20	20	20	21	21	21	22
	Query ce Match Length DB II	31	31	31	31	31	31	31	31	31
	Query	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
	Score	174	174	174	174	174	174	174	174	174
	Result No.	-	8	e	4	ហ	9	7	80	6

Prolactin relea.		Peptide production			oxyto	Rat CRH releasing	Peptide production		Rat oxytocin secre	Rat CRH releasing	Peptide production		Rat type G protein	Ξ	oxytoci		bPrRp31 peptide, u	Bovine G protein-c	Bovine pituitary-d	Bovine 19P2 ligand		Bovine oxytocin se	19P2 ligand peptid		Bovine CRH releasi	Bovine PrRP-31 pep	Peptide production			Bovine pituitary-d	Bovine oxytocin se	Bovine CRH releasi	Peptide production		Bovine pituitary-d	
AAB90993	AAB26400	ABU60826	ABU60837	AAW31385	AAB10356	AAG62525	ABU60838	AAW31386	AAB10357	AAG62526	ABU60839	AAW95172	AAW31383	AAW97225	AAB10354	AAG62523	AAB73370	AAW31371	AAW97218	AAW87613	AAW95188	AAB10347	AAY49290	AAY49298	AAG62516	AAE26399	ABU60825	ABU60831	AAW31372	AAW95189	AAB10348	AAG62517	ABU60832	AAW31373	AAW95190	
22	23	24	24	18	21	22	24	18	21	22	24	20	18	50	71	22	55	18	50	50	20	21	21	21	55	53	24	24	18	20	71	22	24	18	20	
31	31	31	31	32	35	32	32	33	33	33	33	82	83	83	83	83	31	31	31	31	31		31	31		31					32	32	32	33	33	
100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	94.3	93.7	93.7	93.7	93.7	93.7	93.7	93.7	93.7	•	93.7			•	93.7	93.7	93.7	93.7	93.7	
174	174	174	174	174	174	174	174	174	174	174	174	174	174	174	174	174	164	163	163	163	163	163	163	163	163	163	163	163	163	163	163	163	163	163	163	
10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	53	30	31	32	33	34	35	36	37	38	38	40	41	42	43	44	4.5	

ALIGNMENTS

RESULT 1 AAW31384 AAW31384;

AAW31384 standard; Peptide; 31 AA.

(first entry) 06-APR-1998 Rat type G protein-coupled receptor ligand fragment 1.

G protein-coupled receptor; ligand binding; pharmaceutical; modulator; pituitary; central nervous system; pancreas; prophylactic; therapeutforagent.

MQ9724436-AZ RAE BD.

10-Jun-1997

96WO-JP03821. 26-DEC-1996;

95JP-0343371. 96JP-0059419. 96JP-0211805. 96JP-0246573, 18-SEP-1996; 28-DEC-1995; 15-MAR-1996; 12-AUG-1996;

(TAKE) TAKEDA CHEM IND LTD

Новоуа М; Pujii R, Fukusumi S, Habata Y, Hinuma S, Kawamata Y, Kitada C, Use of G protein-coupled receptor ligands - for modulating prolactin secretion or placental function, e.g. for treating menopausal syndrome, tumours, autoimmune disease or abnormal pregnancy

WPI; 1999-105614/09

Claim 3, Page 153; 241pp; English

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This sequence represents a peptide fragment from a novel rat type
ligand polypeptide corresponding to amino acid residues 22 to 52 of the
sequence represented in AAW31383 and is used in an assay) to monitor
ligand binding to the G protein-coupled receptor protein. Pharmaceutical
compositions containing this ligand may be used as a pituitary function
modulator, a central nervous system modulator or a pancreatic function
compositions containing this ligand may be used as a pituitary function
modulator. This ligand could have specific applications as a
prophylactic or therapeutic agent for dementia, depression, hyperkinetic
crauma, growth hormone secretory disease, hyper- and polyphagia,
trauma, protein hormone secretory disease, hyper- and polyphagia,
hyperliphdaemia, hypercholesterolaemia, hyperglyceridaemia,
hyperprolactinaemia, diabetes, cancer, pancreatitis, renal disease,
hyper is syndrome, neurosis, asthma, rheumatoid arthritis, spinal injury,
transient brain ischaemia, epilepsy, amylotrophic lateral sclerosis,
acute myocardial infarction, infertility, spinocerebellar degeneration,
cotte myocardial infarction, infertility, spinocerebellar degeneration,
oligogalactia. Assays can also be developed to screen compounds which are
capable of altering the binding activity of the ligand affecting
activation of the G protein-coupled receptor protein.
                                                                            Ligand peptide for G protein-coupled receptor - acts by modulating function in the central nervous system, pancreas and pituitary gland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 31,
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100.0%; Pred. No. 1.8e-18;
ive 0; Mismatches 0;
                                                                                                                                                            Claim 2; Page 179; 258pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.0
----hes 31; Conservative
WPI; 1997-363672/33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31 AA;
                         N-PSDB; AAV02421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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The present sequence represents a rat type ligand fragment. It is used in the course of the invention. The specification describes an agent for modulating prolactin secretion which comprises a ligand polypeptide or a salt, for a 6 protein-coupled receptor (GPCR) controlled to the secretion of the secretion can be used for treating or preventing hypocovarianism, gonecyst cacogenesis, menopausal syndrome, enthyroid or hypometabolism. They can by used for promoting syndrome, enthyroid or hypometabolism. They can by used for promoting syndrome, enthyroid or hypometabolism. They can by used for promoting prolactin secretion can be used for treating or preventing pituitary adenomatosis, brain tumour, emmenlopathy, autoimmune disease, prolactinoma, infertility, impotence, amenorthea, galactorrhea, cromegaly, Chlari-Frommel syndrome, sheehan syndrome or dyszoospermia. The inhibitory agents can also be used as contraceptives. The agents for modulating placental function can be used for treating or preventing choriccarcinoma, hydatid mole, irruption mole, abortion, unthirity fetus, abnormal saccharometabolism, abnormal lipidmetabolism or oxytocia.

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Gaps

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Indels

/ Match 100.0%; Score 174; DB 20; Local Similarity 100.0%; Pred. No. 1.8e-18; He 31; Conservative 0; Mismatches 0;

Best Loc Matches

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Gaps ö

IndelB

31 AA;

Sequence Query Match 1 SRAHQHSMETRTPDINPAWYTGRGIRPVGRF 31

Length 31;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rat type ligand; modulation; prolactin secretion; g protein-coupled receptor; GPGR; hypocvarianism; gonecyst cacogenesis; menopausal syndrome; euthyroid; hypometabolism; lactation; pitultary adenomatosis; brain tumour; emmeniopathy; autoimmune disease; prolactinoma; infertility; impocence; amenorhaa; galactorrhea; acromegaly; Chiari-Frommel syndrome; Argonz-del Castilo syndrome; Porbes-Albright syndrome; lymphoma; Sheehan syndrome; dyszonopermia; contraceptive; placental function; choriocarcinoma; hydatid mole; irruption mole; abortion; unthrifty fetus; abnormal saccharometabolism; abnormal lipidmetabolism; oxytocia.
                                      31
                                                                         SRAHOHSMETRTPDINPAWYTGRGIRPVGRF 31
                                  SRAHOHSMETRTPDINPAWYTGRGIRPVGRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rat type ligand polypeptide fragment.
                                                                                                                                                                                                                                                                                         AAW97233 standard; peptide; 31 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                            06-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                       AAW97233;
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RESULT

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Kawamata Y, Matsumoto H;

(TAKE) TAKEDA CHEM IND LTD

Fujii R, Hinuma S,

98WO-JP02765 97JP-0165437

22-JUN-1998; 23-JUN-1997;

WO9858962-A1 30-DEC-1998.

Rattus sp

AAW97233

XX
AC
AAW
AC
XX
AC
XX
AC
XX
XX
AC
XX
XW
AC
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Producing a 19P2 pituitary G protein receptor ligand - by cleavage of a fusion protein, useful for preventing and treating dementia, breast cancer, renal failure and autoimmune disease
                                                                                                                                                   19P2 ligand, G protein coupled receptor, pituitary, prolactin releasing peptide, rat, dementia, breast cancer,
                                                                                                                                                                                                                                                                                                                                   Tanaka Y;
1 SRAHOHSMETRTPDINPAWYTGRGIRPVGRF
                                                                                                                                                                                                                                                                                                                                   Suenaga M,
                                                             AAW87614 standard; Peptide; 31 AA
                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 5; Page 34; 56pp; English.
                                                                                                                                                                                                                                                                 98EP-0111725.
                                                                                                                                                                                                                                                                                       97JP-0172118
                                                                                                                                                                                                                                                                                                             (TAKE ) TAKEDA CHEM IND LTD
                                                                                                         29-MAR-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                   Moriya T, Nishimura O,
                                                                                                                                                                                                                                                                                                                                                        WPI; 1999-047884/05.
                                                                                                                                Rat 19P2 ligand
                                                                                                                                                                                                                                                                 25-JUN-1998;
                                                                                                                                                                                                                                                                                       27-JUN-1997;
                                                                                                                                                                                                                    EP887417-A2
                                                                                                                                                                                                                                           30-DEC-1998
                                                                                                                                                                                               Rattus sp.
                                                                                   AAW87614;
                                                                                                                                                                          therapy.
                                       RESULT 3
                                                   AAW87614
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GPRIO; UHR-1; modularor; pituitary; central nervous system; pancreas; tissue; screen; therapeutic; binding; senile dementia; ligand; murine; tablatimer; disease; Parkinson's disease; Huntington's disease; drug; Creutzfeld-Jakob disease; poisoning; schizophrenia; growth hormone; secretion; diabetes; cancer; rheumatoid arthritis; epilepsy; vasopressor; gene therapy; transgenic animal.
                            This is the amino acid sequence or the rat piturary of protein-coupled receptor ligand 1972L. A method suitable for commercial high-level production of 1972L comprises expressing the ligand in host cells as a recombinant fusion protein e.g. with human basic fibroblast growth factor (see AANS194-95) that has been modified to include an N-terminal cysteine residue. The ligand is released from the fusion by cyanylation followed by ammonolysis. 1972L has prolactin secretion-inhibiting properties. It can be used in the treatment and prevention of various diseases including senile dementia, cerebrovascular dementia, and dementia associated with; genealogical disease, Huntington's disease, infectious disease, cerebrovascular dementia, and dementia associated with; genealogical disease, Huntington's disease), infectious disease, coxicosis (e.g. Arabeimer's disease, proxicosis (e.g. hypothyroidism, vitamin Bl2 deficiency, alcoholism, intoxication by drugs, metal and organic compounds), tumourigenic subarachnoidal heamorrhage, and other types of dementia, depression, hyperactive child syndrome (microencephalopathy) and disturbance of consciousness. It is also useful for prevention and treatment of disease associated with prolactin hype and hypersecretion respectively, including: hyperprolactinamal, pituitary adenoma, breast cancer, infertility, impotence and autoimmune disease

(Mypersecretion disorders), and seminal vesicle hypoplasia, osteoporosis, menopausal syndrome and renal failure (hyposecretion reagent for grady of the proplactin secretory function or as a test and a seminal reagences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pituitary-derived ligand polypeptide, G-protein coupled orphan receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 31;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                   This is the amino acid sequence of the rat pituitary G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 174; DB 20; 100.0%; Pred. No. 1.8e-18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            lactogogue in mammalian farm animals.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 100.
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Matches
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(TAKE) TAKEDA CHEM IND LTD.

Fukusumi S, Hinuma S;

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This represents the matured murine pituitary-derived ligand polypeptide sequence. The polypeptide is a ligand for the G-protein coupled orphan receptor designated GPR10 (human) or UHR-1 (rat). Cells transformed with a vector containing the ligand polypeptide encoding DNA are used to produce a recombinant ligand polypeptide. The ligand polypeptide, and its fragments, modulate function of the pituitary, central nervous system, pancreas and other tissues and can be used to screen for agents that modulate binding of the polypeptide to the receptor; to quantify the modulate binding of the polypeptide to the receptor; to quantify the modulate binding of the polypeptide and to raise antibodies. They may also be used therapeutically, e.g. to treat senile dementia; Alzheimer's poisoning by heavy metals or drugs; diabetes; schizophrenia; disorders of growth hormone secretion; cancer; rheumatoid arthritis, epilepsy and many others, also to improve post-operative nutritional status and as contest, also to improve post-operative nutritional status and as the mutein are used to study the function of the polypeptide encoding DNA or its mutein are used to study the function of the polypeptide encoding on and primers; to identify related sequences; in receptor-binding assays; for production of Ab and antisers; in drug development; for gene therapy, and to develop transgenic animals.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GPRIO; UHR-1; modulaTor; pituitary; central nervous system; pancreas; tissue; screen; therapeutic; binding; senile dementia; ligand; murine; Alabelmer's disease; Parkinson's disease; huntington's disease; drug; Creutzfeld-Jakob disease; poisoning; schizophrenia; growth hormone; secretion; diabetes; cancer; rheumatoid arthritis; epilepsy; vasopressor; gene therapy; transgenic animal; epitope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pituitary-derived ligand polypeptide; G-protein coupled orphan receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                  New polypeptide ligand for orphan G protein coupled receptors - for treating disorders of central nervous system, pituitary and pancreas, and for drug screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Murine pituitary-derived ligand polypeptide antigenic epitope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 174; DB 20; Length 31; 100.0%; Pred. No. 1.8e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 SRAHQHSMETRTPDINPAWYTGRGIRPVGRF 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                       Disclosure, Page 134; 206pp; English.
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WPI; 1999-009423/01.
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WPI; 1999-009423/01

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The invention relates to a murine pituitary-derived ligand polypeptide which is a ligand for the G-protein coupled orphan receptor designated GPR10 (human) or UHR-11 (rat). Cells transformed with a vector containing the ligand polypeptide encoding DNA are used to produce a recombinant ligand polypeptide. The ligand polypeptide, and its fragments, modulate function of the pituitary, central nervous system, pancreas and other crises and can be used to screen for agents that modulate binding of the polypeptide to the receptor; to quantify the amount of receptor in a sample and to rasks antibodies. They may also be used therapeutically, e.g. to treat senile dementia; Alzheimer's Parkinson's or Huntington's disease; Creutzfeld-Jakob disease; poisoning by heavy metals or drugs; cheuratoid arthritis, epilepsy and many others, also to improve post-coperative nutritional status and as vasopressor. Transgenic animals carrying the ligand polypeptide encoding DNA or its mutein are used to study the function of the polypeptide expressing genes as models of disease, for drug screening and as source of cell lines. The ligand polypeptide coperative mutaits as a source of probes and primers; to identify criatsers; in drug development; for gene therapy and to develop criatisera; in drug development, for gene therapy and to develop artisera; in drug developments APM95174 to AAM95178 represent antigenic principles which can be used for the preparation of anti-ligand polypeptide production of the preparation of anti-ligand polypeptide.
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                                       r orphan G protein coupled receptors - used central nervous system, pituitary and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rat oxytocin secretion promoting peptide SEQ ID NO: 18.
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100.0%; Pred. No. 1.8e-18;
ive 0; Mismatches 0;
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                                                                                                                    Disclosure; Page 26; 206pp; English
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                                   New polypeptide ligand for orphar for treating disorders of central pancreas, and for drug screening
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Best Local Similarity 100.
Matches 31, Conservative
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The invention relates to a method for identifying compounds useful for modulating body weight. The method comprises cell-free and/or cell-based
                                                                                                                    This invention describes a novel oxytocin secretion-regulating agent which contains a ligand peptide or its salt for the G protein-coupled receptor protein. It is useful in the form of drugs for ameliorating, preventing and treating diseases relating to oxytocin secretion e.g. weak pains and atonic bleeding, before and after expulsion of placenta, uterine recovery failure, caesarean section, stoppage of artificial fertilization or galactostasis and is also applicable in veterinary medicine for promoting milk production in cow, goat and pig. This sequence represents a rat peptide which acts as an oxytocin secretion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Identifying modulators of body weight by a combination of a cell-free or cell-based assay to identify modulators of GPR10, followed by an in vivo assay for the compounds effect on e.g. feeding behavior -
             Physiologically-active polypeptide recognized as ligand by G
protein-coupled receptor protein, for promoting secretion of oxytocin,
as drugs for diseases relating to oxytocin secretion and in veterinary
medicine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Prolactin-releasing peptide; PTRP; GPR10; G protein-coupled receptor; feeding behaviour; food intake; modulation; antagonist; anorectic; obesity; agonist; cachexia.
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100.0%; Pred. No. 1.8e-18
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0; Mismatches
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                                                                                            72pp; Japanese
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                                                                                              Claim 3; Page 57;
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Length 31; Indels

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assays that identify compounds which bind to and/or activate or inhibit the activity of GPR10, a G protein-coupled receptor. These assays are then followed by an in vivo assay of the effect of the compound on feeding behaviour, body weight or metabolic rate in a mammal. Prolactinreleasing peptide (PrRP; AAY87504) is a ligand of GPR10. Binding of PrRP to GPR10 stimulates a signal transduction cascade, which results in an increase in food intake. Compounds identified using the method of the invention are useful for the modulation of body weight. Antagonists of GPR10 can be used to treat obesity, while GRR10 agonists can be used to treat cachexia. The present sequence represents rat PrRP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention provides a monoclonal antibody which has a specific reaction with the part peptide of the C-terminal of 19P2 ligand or its derivative. The antibodies can be used in diagnosis or to treat or prevent diseases associated with abnormality in the pituitary function regulatory mechanism (e.g. promotion of prolactin secretion), central nervous regulatory mechanism, and pancreatic function regulatory mechanism, and pancreatic function regulatory electronism. The antibody-based immunoassay can also be applied in clarifying the physiological functions of the ligand and its derivative Sequences AAX49290-302 represent peptide fragments of the 19P2 ligand.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antibody; 19P2 ligand; diagnosis; prolactin secretion; regulatory mechanism; central nervous system; pancreatic.
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Best Local Similarity
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Modified-site
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Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypercortisolaemia, secondary or chronic hypoadremocorticism, Addison's disease (including boreadom, nausea, pigmentation, hypogonadism, hair loss, and hypotension), adrenal gland hypofunction and obesity. The present sequence is a peptide used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence describes a method of controlling the secretion of
                                                                                                                                                                                                                                                                          Rat, corticotrophin releasing hormone, CRH; G protein receptor ligand; analgesic; hyperaldosteronism; hypercortisolaemia; hyperalcism; Addison's disease; adrenal gland hyperfunction; obesity.
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                    0; Indels
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       Pred. No. 1.8e-18;
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                                                                                                                                                        AAG62524 standard; peptide; 31
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26-SBP-2000; 2000JP-0297073.
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Matches 31, Conserv
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Best Local Similarity
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                                                                                                                                                                                      AAG62524;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB90993 ;
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                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes a modified therapeutic peptide (I) comportsing a therapeutically active amino acid region (III) and a reactive group (II) (e.g. succinimidyl and maleimido groups) attached to a less therapeutically active amino acid region (IV), which covalently bonds with amino/hydroxyl/thiol groups on blood components to form a peptidase stabilised therapeutic peptide composed of 3-50 amino acids. (I) are useful for modifying therapeutic peptides e.g. hormones, growth factors and neurotransmitters, to protect them from peptidase activity in vivo for the treatment of various disorders. Endogenous therapeutic peptides are not suitable as drug candidates as they require frequent administration due to rapid degradation by peptidases in the body. Modifying and attaching therapeutic peptides to albumin prevents or reduces the action of peptidases to increase length of activity (half infa and specificity as bonding to large molecules decreases the action of peptidases to increase length of activity (half intracellular uptake and interference with physiological processes. ABB90829 to ABB92441 represent peptides which can be used in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rat; wakefulness; sleep disorder; prolactin releasing peptide receptor;
PrRP; GPR10; therapy; epilepsy; narcolepsy; sleepiness; sleep apnoea;
                                                                                                                                                                                                                                                                                                                          Modifying and attaching therapeutic peptides to albumin prevents peptidase degradation, useful for increasing length of in vivo activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gape
                                 Protection, endogenous therapeutic peptide; peptidase; conjugation, blood component; modification; succinimidyl; maleimido group; amino; hydroxyl; thiol; hormone; growth factor; neurotransmitter.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 31;
                                                                                                                                                                                                                                                                        Thibaudeau K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 174; DB 22; 100.0%; Pred. No. 1.8e-18;
                                                                                                                                                                                                                                                                         Holmes DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SRAHQHSMETRTPDINPAWYTGRGIRPVGRF 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SRAHQHSMETRTPDINPAWYTGRGIRPVGRF 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
           Prolactin releasing peptide SEQ ID NO:167.
                                                                                                                                                                                                                                                                                                                                                                           Disclosure, Page 244; 733pp; English.
                                                                                                                                                                                                                                                                          Bridon DP, Ezrin AM, Milner PG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAE26400 standard; peptide; 31 AA
                                                                                                                                                                                              99US-0134406.
99US-0153406.
99US-0159783.
                                                                                                                                                                        17-MAY-2000; 2000WO-US13576.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31; Conservative
                                                                                                                                                                                                                                                  (CONJ-) CONJUCHEM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rat PrRP-31 peptide.
                                                                                                                                                                                                                                                                                                WPI; 2001-112059/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31 AA;
                                                                                                                        WO200069900-A2
                                                                                     Homo sapiens.
                                                                                                                                                                                                            10-SEP-1999;
15-OCT-1999;
                                                                                                                                                                                                17-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-DEC-2002
                                                                                                                                                 23-NOV-2000
                                                                                                  Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAE26400;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 11
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The present invention relates to a method of screening for compounds for promoting wakefulness or sleep in a mammal. The method involves administering a prolactin releasing peptide (PrR) receptor (GPR10) agonist or antagonist respectively and determining the ability of the compound to promote wakefulness or sleep. The compounds identified from the method are used in the therapy of epilepsy and other diseases associated with absence seizures and in promoting wakefulness and sleep in individuals having sleep disorders such as insomnia and narcolepsy. PrRP receptor agonists may be used to treat common disorders which lead to sleeplness, e.g. sleep apnoea, narcolepsy, idlopathic hypersomnia and psychogenic hypersomnia. PRRP receptor antagonists are useful for promoting sleep and for treating insomnia such as adjustment sleep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Screening for compounds useful for promoting wakefulness or sleep, and for treating sleeping disorders, e.g. insomnia, hypersomnia or sleep apnea, comprises administering a prolactin releasing peptide agonist or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          disorder and psychophysiologic insomnia. The present sequence is rat PrRP-31 peptide.
insomnia, idiopathic hypersomnia; psychogenic hypersomnia; seizure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peptide production by gene recombination associated peptide #10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peptide production; low-molecular peptide; KiSS-1; GPRB ligand;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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100.0%; Score 174; DB 23;
Best Local Similarity 100.0%; Pred. No. 1.8e-18;
Matches 31; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 SRAHQHSMETRTPDINPAWYTGRGIRPVGRF 31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-MAY-2002; 2002WO-JP04735.
                                                                                                                                                                                                                                                                                                      17-AUG-2001; 2001US-0932161.
                                                                                                                                                                                                                                                                                                                                                                     28-APR-2000; 2000US-0560915.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-403931/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene recombination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Civelli O, Lin S;
                                                                                                                                                                                                                                                                                                                                                                                                                                   (CIVE/) CIVELLI O. (LINS/) LIN S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31 AA;
                                                                                                                                                                   US2002037533-A1
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                                         anticonvulgant.
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                                                                                                                                                                                                                                        28-MAR-2002.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antagoniet
                                                                                                    Rattus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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ABU60826
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The invention describes a method of producing a peptide comprising the excision of the N and C-terminals of a target peptide with enzymes or chemically through the attached cleavage sites repeated by ligation in a precursor protein. The method is for producing (low-molecular) peptides e.g. KiSS-1 peptide and GRR8 ligand for subsequent applications by the gene recombination technique through tandem repeats to provide a precursor protein with specific cleavage sites. With this method, peptide production can be carried out easily to provide large quantities of the required peptides. This is the amino acid sequence of a peptide associated with the peptide production method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Process for producing peptides e.g. KiSS-1 peptide and GPR8 ligand for subsequent applications by gene recombination technique through tandem repeats to provide precursor protein with specific cleavage sites
                                                                                                                                          Process for producing peptides e.g. KiSS-1 peptide and GPR8 ligand for subsequent applications by gene recombination technique through tandem repeats to provide precursor protein with specific cleavage sites -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention describes a method of producing a peptide comprising the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peptide production by gene recombination associated peptide #21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   production; low-molecular peptide; KiSS-1; GPR8 ligand;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 174; DB 24; 100.0%; Pred. No. 1.8e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 SRAHQHSMETRTPDINPAWYTGRGIRPVGRF 31
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                                                                              Kitada C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                Disclosure; Page 58; 87pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 64; 87pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Suenaga M, Ito T,
                                                                                Suenaga M, Ito T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABU60837 standard; Peptide; 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-MAY-2002; 2002WO-JP04735.
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               17-MAY-2001; 2001JP-0147341
                                               (TAKE ) TAKEDA CHEM IND LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                             WPI; 2003-129302/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene recombination
                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 31 AA;
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                                                                                Nishimura O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31;
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excision of the N and C-terminals of a target peptide with enzymes or chemically through the attached cleavage sites repeated by ligation in a precursor protein. The method is for producing ilow-molecular) peptides e.g. KisS-1 peptides ilgand for subsequent applications by the gene recombination technique through tandem repeats to provide a precursor protein with specific cleavage sites. With this method, peptide production can be carried out easily to provide large quantities of the required peptides. This is the amino acid sequence of a peptide associated with the peptide production method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   G protein-coupled receptor; ligand binding; pharmaceutical;
modulator; pituitary; central nervous system; pancreas; prophylactic;
therapeutic agent.
                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                     Length 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pujii R, Fukusumi S, Habata Y, Hinuma S, Hosoya M;
Kawamata Y, Kitada C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rat type G protein-coupled receptor ligand fragment 2.
                                                                                                                                                                                                                     100.0%; Score 174; DB 24; 100.0%; Pred. No. 1.8e-18;
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                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                             1 SRAHQHSMETRIPDINPAWYTGRGIRPVGRF
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95JP-0343371.
96JP-0059419.
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                                                                                                                                                                                                                                                          31; Conservative
                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (PI; 1997-363672/33
                                                                                                                                                                                    31 AA;
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15-MAR-1996;
12-AUG-1996;
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                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW31385;
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                                                                                                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                   RESULT 14
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Turner's syndrome, neurosis, asthma, rheumatoid arthritis, spinal injury, transient brain ischaemia, epilopsy, amylotrophid. lateral sclerosis, acute myocardial infarction, infertility, spinocerebellar degeneration, bone fracture, trauma, atopic dermatitis, osteoporosis and/or oligogalactia. Assays can also be developed to screen compounds which are capabbe of altering the binding activity of the ligand affecting activity activity of the ligand affecting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CO€
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This invention describes a novel oxytocin secretion-regulating agent which contains a ligand peptide or its salt for the g protein-coupled receptor protein. It is useful in the form of drugs for ameliorating, preventing and treating diseases relating to oxytocin secretion e.g. weak pains and atonic bleeding, before and after expulsion of placenta, uterine recovery failure, caesarean section, stoppage of artificial fertilization or galactostasis and is also applicable in veterinary medicine for promoting milk production in cow, goat and pig. This sequence represents a rat peptide which acts as an oxytocin secretion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rat; oxytocin secretion promoter; G protein-coupled receptor protein; treatment; disease; pain; atonic bleeding; uterine recovery failure; ccessarean section; artificial fertilization; galactostasis; goat; pig; veterinary medicine; milk production.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Physiologically-active polypeptide recognized as ligand by G protein-coupled receptor protein, for promoting secretion of oxytocin, as drugs for diseases relating to oxytocin secretion and in veterinary medicine.
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                                                                                                                                                                       100.0%; Score 174; DB 18; Length 32; 100.0%; Pred. No. 1.8e-18; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rat oxytocin secretion promoting peptide SEQ ID NO: 19.
                                                                                                                                                                                                                                        Disclosure; Page 57; 72pp; Japanese.
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                                                                                                                                                                                       Best Local Similarity 100.
Matches 31, Conservative
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                                                                                                                                        32 AA;
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Gaps

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Length 32; Indels

Query Match 100.0%; Score 174; DB 21; Best Local Similarity 100.0%; Pred. No. 1.8e-18; Matches 31; Conservative 0; Mismatches 0;

33, Appl 1, Appli 44, Appl 115, App 117, App 122, App 131, App

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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 8, Application US/09105678A

Patent No. 6103882

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Moriya, Takeo
APPLICANT: Hanaka, Yoko
ITILE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Riopy disk
COMPUTER: READABLE FORM:
MEDIUM TYPE: Picpy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,678A
FILING DATE: 26-JUN-1998
PRIOR APPLICATION NUMBER: US/09/105,678A
ATPONEY/AGENT INFORMATION:
NAME: COMIIN: David G.
REGISTRATION NUMBER: 27,026
REGISTRATION NUMBER: 27,026
REGISTRATION NUMBER: 27,026
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAK: 617-523-3400
US-09-105-678A-33
US-08-776-971-7
US-08-742-108-33
US-08-76-971-115
US-08-776-971-115
US-08-776-971-115
US-08-776-971-112
US-08-776-971-131
US-08-776-971-131
US-08-776-971-31
US-08-776-971-33
US-09-105-678A-29
US-09-421-208-29
US-09-105-678A-3
US-09-105-678A-3
US-09-105-678A-3
US-09-105-678A-3
US-09-105-678A-3
US-09-421-208-9
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                                                                                                                                                                                                                                                                                                                                                               ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 617-523-6440 INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 31 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.
Matches 31; Conservative
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MOLECULE TYPE: peptide
   CITY: Boston
STATE: MA
COUNTRY: USA
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7, Appli
31, Appl
5, Appli
97, Appli
7, Appli
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114.055 Million cell updates/sec
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Sequence 4
Sequence 3
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Sequence
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(cgn2_6/ptodata/1/iaa/PcTuS_COMB.pep:*
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                      GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-60-915-14
US-09-100-678A-34
US-09-100-678A-34
US-09-100-678A-38
US-09-100-678A-39
US-09-105-678A-39
US-09-776-971-45
US-08-776-971-124
US-08-776-971-124
US-08-776-971-137
US-09-105-678A-31
US-09-105-678A-31
US-09-776-971-137
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US-09-776-971-5
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Maximum Match 100%
Listing first 45 summaries
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Gaps

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Kawanta, Yaji
Hosoya, Masaki
Pujii, Ryo
Pujii, Ryo
Fukusumi, Shoji
Kitada, Chieko
INTER OF INVENTION: POLYPROTEINS, THRIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS:
ADDRESSER: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
CITY: Boston
                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 174; DB 3; Length 31;
                                                                                           Length 31;
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ZIP: 01109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEG for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06-Feb-1997
CLASSIFICATION: <Unknown>
                                                                                         100.0%; Score 174; DB 3; 100.0%; Pred. No. 1.1e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: PCT/JP96/03821
PILING DATE: 28-DEC-1996
APPLICATION NUMBER: DT //34331
PILING DATE: 28-DEC-1995
APPLICATION NUMBER: JP 8/59419
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: 12-AUG-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: CONLIN, DAYIG G.
REFERENCE/POCKET NUMBER: 27,026
                                                                                                                                                                                                               1 SRAHQHSMETRTPDINPAWYTGRGIRPVGRF 31
                                                                                                                                                                                     1 SRAHQHSMETRIPDINPAWYTGRGIRPVGRF 31
                                                                                                                                       0; Mismatches
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                                                                                                                                                                                                                                                                                                         SSULT 4
S-08-776-971-47
S-08-776-971-47
Sequence 47, Application US/08776971B
Patent No. 6228984
GENERAL INFORMATION:
APPLICANT: Hinuma, Shuji
Habata, Yugo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 617-523-6440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
                                                                                           Query Match
Best Local Similarity 100.
Matches 31, Conservative
1 TYPE: PRT
7 ORGANISM: Mus musculus
US-09-172-353-4
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Parent No. 6197530
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Stricker-Kongra, Alain
APPLICANT: Stricker-Kongra, Alain
APPLICANT: GL, Wei
TITLE OF INVENTION: GPR10 AS A TARGET FOR IDENTIFYING WEIGHT MODULATING COMPOUNDS
FILE REFERENCE: 07334/102001
CURRENT APPLICATION NUMBER: US/09/172,353
CURRENT FILING DATE: 1998-10-14
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 4
LENGTH: 31
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                                                                                                                                                                              GENERAL INPORMATION:
APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Manaka, Yoko
APPLICANT: Nishimura, Osamu
ITILE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UNMER: US/09/105,678A
FILING DATE: 26-JUN-1998
PRIOR APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
100.0%; Score 174; DB 3;
Best Local Similarity 100.0%; Pred. No. 1.1e-19;
Matches 31; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 SRAHOHSMETRTPDINPAWYTGRGIRPVGRF 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 SRAHOHSMETRTPDINPAWYTGRGIRPVGRF 31
Sequence 37, Application US/09105678A
Patent No. 6103882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Conlin, David G.
REGISTRATION NUMBER: 27,026
REFRENCE/DOCKET NUMBER: 4846
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-105-678A-37
                                                                                                                    US-09-105-678A-37
                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: MA
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US-09-172-353-4
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| Sequence 14, Application US/09560915 | Patent No. 6383764 |
| GENERAL INFORMATION: | Patent No. 6383764 |
| GENERAL INFORMATION: | Patent Seven |
| APPLICANT: Civelli, Olivier |
| APPLICANT: Lin, Steven |
| TITLE OF INVENTION: Therapeutic Compositions and Methods |
| TITLE OF INVENTION: Therapeutic Compositions and Methods |
| TITLE OF INVENTION: Teleting To Prolactin Releasing Peptide (PRRP) |
| FILE REFERENCE: P-UC 3534 |
| CURRENT APPLICATION NUMBER: US/09/560,915 |
| CURRENT PILING DATE: 2000-04-28 |
| SOFTWARR OF SEQ ID NOS: 24 |
| SOFTWARR: FastSEQ for Windows Version 4.0 |
| SEQ ID NO 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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100.0%; Score 174; DB 3; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.1e-19;
Matches 31; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 31;
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TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND WIMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSE DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP STREET: 130 Water Street
CITY: Boston
STATE: WA
COUNTRY: USA
                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: PROFILE PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/421,208
FILING DATE:
PRIOR APPLICATION NUMBER: US/09/421,208
FILING DATE: 26-JUN-1998
APPLICATION NUMBER: US 09/105,678
FILING DATE: 26-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: CONIIn, David G.
REGISTRATION NUMBER: 27,006,678
REGISTRATION NUMBER: 27,006,678
REGISTRATION NUMBER: 27,006,678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.0%; Pred. No. 1.1e-19;
Matches 31; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 SRAHQHSMETRTPDINPAWYTGRGIRPVGRF 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 SRAHQHSMETRIPDINPAWYTGRGIRPVGRF 31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 48466-342
TELECOMMUNICATION INFORMATION:
TELEBRIONE: 617-523-3400
TELEBRAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 37:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Rattus
US-09-560-915-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-421-208-37
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                                   Indels
                                                                                                                                                                                                                                                                                                                                           APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Tanaka, Yoko
APPLICANT: Mishimura, Osamu
IITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYRE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/421,208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, STREET: 130 Water Street
CITY: Boston
     Best Local Similarity 100.0%; Pred. No. 1.1e-19; Matches 31; Conservative 0; Mismatches 0;
                                                                                                                        1 SRAHQHSMETRTPDINPAWYTGRGIRPVGRF 31
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                                                                                    1 SRAHQHSMETRIPDINPAWYTGRGIRPVGRF 31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: COLLIN, DAVIG G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48466-342
TELEPCOMMUNICATION INPORMATION:
TELEPHONE: 677-523-3400
INPORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/105,678
FILING DATE: 26-JUN-1998
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 37, Application US/09421208
Patent No. 6258561
GENERAL INFORMATION:
APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
                                                                                                                                                                                                                                                                 Sequence 8, Application US/09421208
Patent No. 6258561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , MOLECULE TYPE: peptide US-09-421-208-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
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TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS:
ADDRESSEE DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
                                                                                                                 Length 32;
                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06-Feb-1997
CLASSIFICATION: <Unknown>
                                                                                                       100.0%; Score 174; DB 3;
illarity 100.0%; Pred. No. 1.1e-19;
Conservative 0; Mismatches 0:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP96/03821
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: UP 7/343371
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: UP 8/59419
FILING DATE: 15-WAR-1996
APPLICATION NUMBER: UP 8/211805
FILING DATE: 12-AUG-1996
APPLICATION NUMBER: UP 8/246573
FILING DATE: 18-SEP-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                          1 SRAHQHSMETRIPDINPAWYTGRGIRPVGRF 31
                                                                                                                                                                                                                                                        1 SRAHOHSMETRTPDINPAWYTGRGIRPVGRF 31
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US-08-776-971-48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Conlin, David G.
REGISTATION UNDERS: 27,026
REFERENCE/DOCKET NUMBER: 47176
TELECOMMUNICATION INFORMATION:
TELEFAX: 617-523-3400
INFORMATION FOR SRQ ID NO: 48:
                                                                                                                                                                                                                                                                                                                                          NS-08-776-971-48
Sequence 48, Application US/08776971B
Patent No. 6228984
GENERAL INFORMATION:
APPLICANT: Hinuma, Shuji
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Habata, Yugo
Kawamata, Yuji
Hogoya, Magaki
Pujii, Ryo
Fukusumi, Shoji
                     TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-105-678A-38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
                                                                                                                                    Similarity
  STRANDEDNESS
                                                                                                                 Query Match
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Matches
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                                                                                                       Sequence 4, Application US/0979955

Bacent No. 6537765

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Stricker-Kongra, Alain
APPLICANT: GL, Wei
TITLE OF INVENTION: GFRIO AS A TARGET FOR IDENTIFYING WEIGHT MODULATING COMPOUNDS
FILE REFERENCE: 07334/102001
CURRENT APPLICATION NUMBER: US/09/799, 955
CURRENT FILING DATE: 2001-03-06
PRIOR FILING DATE: 1998-10-14
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSEQ for Windows Version 3.0
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Patent No. 6103882
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SECURNCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,678A
FILING DATE: 26-JUN-1998
PRIOR APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGRNT INFORMATION:
SRAHQHSMETRTPDINPAWYTGRGIRPVGRF 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SRAHQHSMETRIPDINPAWYTGRGIRPVGRF 31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
100.0%; Score 174; D
Best Local Similarity 100.0%; Pred. No. 1.1
Matches 31; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Conlin, David G.
REGISTRATION NUMBER: 27,026
REFRENCE/DOCKET NUMBER: 4846
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 31
TYPE: PRT
CRGANISM: Mus musculus
US-09-799-955-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Boston
STATE: MA
COUNTRY: USA
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HOSOYA, MASSAÍ
Fujii, Ryo
Fujii, Ryo
Fukusumi, Shoji
Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSER: DIKE, BROMSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
CITY: BOSEON
                                                                                                                                                                                                                                   WEDIUM TYPE: FOLDER COMPATIBLE
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,678A
FILING DATE: 26-JUN-1998
PRIOR APPLICATION NUMBER: JP 172118/1997
PTILING DATE: 27-JUN-1997
PTILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Conlin, David G.
REGISTRATION NUMBER: 27 0.26
REFERENCE/DOCKET NUMBER: 48466-342
TELECOMMULCATION INFORMATION:
TELECOMMULCATION INFORMATION:
TELECOMMULCATION INFORMATION:
TELECOMMULCATION INFORMATION:
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OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.0%; Pred. No. 1.1e-19;
Matches 31; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 SRAHQHSMETRTPDINPAWYTGRGIRPVGRF 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 SRAHOHSMETRIPDINPAWYTGRGIRPVGRF 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 49, Application US/08776971B Patent No. 6228984 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 130 Water Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Hinuma, Shuji
Habata, Yugo
Kawamata, Yuji
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 39:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 02109
UTER READABLE FORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 33 amino acids
                                                                                                                                  CITY: Boston
STATE: WA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-105-678A-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: MA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-776-971-49
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                                                  Gaps
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    Query Match 100.0%; Score 174; DB 3; Length 32; Best Local Similarity 100.0%; Pred. No. 1.1e-19; Matches 31; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                     Sequence 18, Application US/09421208
| Patent No. 6258561
| GENERAL INFORMATION:
| APPLICANT: Shenaga, Masstco
| APPLICANT: Tanaka, Yoko
| APPLICANT: Hishimura Osamu
| TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
| NUMBER OF SEQUENCES: 52
| NUMBER OF SEQUENCES: 52
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/421,208
                                                                                                                     1 SRAHQHSMETRIPDINPAWYTGRGIRPVGRF 31
                                                                                              1 SRAHQHSMETRTPDINPAWYTGRGIRPVGRF 31
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Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/105,678
FILING DATE: 26-JUN-1998
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-105-678A-39
; Sequence 39, Application US/09105678A
; Patent No. 6103882
; GENERAL INFORMATION:
APPLICANT: Suemaga, Masato
APPLICANT: Moriya, Takeo
; APPLICANT: Tanaka, Yoko
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Conlin, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 4846
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEPHONE: 617-523-6440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: Floppy disk
IBM PC compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , MOLECULE TYPE: peptide US-09-421-208-38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid STRANDEDNESS:
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Best Local
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Gaps

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Length 33; Indels

0; Gaps

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Kiteda, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 174; DB 3; Length 33; 100.0%; Pred. No. 1.1e-19;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: PastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06-Feb-1997
CLASSIFICATION NUMBER: US/08/03821
APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR DATE: 28-DEC-1996
APPLICATION NUMBER: JP 7/343371
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: JP 8/59419
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-AUG-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-AUG-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-AUG-1996
APPLICATION NUMBER: JP 8/216573
FILING DATE: 18-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 SRAHQHSMETRTPDINPAWYTGRGIRPVGRF 31
                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
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REFERENCE/DOCKET NUMBER: 47176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 45, Application US/08776971B Patent No. 6228984 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
NAME: Conlin, David G.
REGISTRATION NUMBER: 27,026
REFRENCE/DOCKET NUMBER: 4846
TELEPROMUNICATION INFORMATION:
TELEPROME 617-523-4400
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
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Hosoya, Masaki
Fujii, Ryo
Fukusumi, Shoji
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Habata, Yugo
                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.0
Matches 31, Conservative
                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
                                                                                                                                                                                                                                                                                                             US-09-421-208-39
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Patent No. 6258561
GENERAL INFORMATION:
APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLON OF INVENTION:
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP STREET: 130 Water Street
STREET: 130 Water Street
STATE: MA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/421,208
PILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.0%; Pred. No. 1.1e-19;
Matches 31; Conservative 0; Mismatches 0;
                                                                                   PRIOR APPLICATION DATA:

PELING DATE: 28-DEC-1996 (03821 PELING DATE: 28-DEC-1996 (03821 PELING DATE: 28-DEC-1996 (03821 PELING DATE: 28-DEC-1995 (03821 PELING DATE: 18-MR-1996 PELING DATE: 18-MR-1996 APPLICATION NUMBER: JP 8/211805 PILING DATE: 18-MC-1996 APPLICATION NUMBER: JP 8/246573 PILING DATE: 18-SEP-1996 ATTORNEY AGENT INFORMATION:

NAMB: COALLIN DAYLG G.

REGISTRATION NUMBER: 27,026

REGISTRATION NUMBER: 27,026

REGISTRATION NUMBER: 27,026

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:
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    APPLICATION NUMBER: US/08/776,971B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear

MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-776-971-49
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APPLICATION NUMBER: US 09/105,678
FILING DATE: 26-JUN-1998
APPLICATION WHERE: JP 172118/1997
FILING DATE: 27-JUN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 33 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 617-523-6440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                       PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
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US-09-421-208-39
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Sequence 88, Appl
Sequence 15, Appl
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Sequence 16, Appl
Sequence 16, Appl
Sequence 14, Appl
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Sequence 14, Application US/09932161

Patent No. US2002003533A1

GENERAL INFORMATION:

APPLICANT: Civelli, Olivier

APPLICANT: Civelli, Olivier

TITLE OF INVENTION: Screening and Therapeutic Methods For TITLE OF INVENTION: Promoting Wakefulness and Sleep

FILE REFERENCE: P-UC 4679

CURRENT APPLICATION NUMBER: US/09/932,161

CURRENT FILING DATE: 2001-08-17

PRIOR APPLICATION NUMBER: US 09/560,915

NUMBER OF SEQ ID NOS: 24

SOFTWARE: FastsEQ for Windows Version 4.0

SEQ ID NO 14
US-09-810-808-7
US-09-820-155-4
US-09-815-242-10994
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US-10-096-777-14
Sequence 14, Application US/10096777
Publication No. US20030171270A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Civelli, Olivier
APPLICANT: Lin, Steven
       TYPE: PRT
ORGANISM: Rattus
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Sequence 1, Appli
Sequence 94, Appl
Sequence 94, Appl
Sequence 13, Appl
Sequence 13, Appl
Sequence 14, Appl
Sequence 14, Appl
Sequence 14, Appl
Sequence 18, Appl
Sequence 18, Appl
Sequence 28, Appl
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256.244 Million cell updates/sec
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                                                                                                      December 3, 2003, 19:11:30 ; Search time 22.5 Seconds
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| cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.ppp:*
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| cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.ppp:*
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                      GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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1 SRAHQHSMETRTPDINPAWYTGRGIRPVGRF 31
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US-10-044-592-4
US-10-044-592-96
US-10-044-592-96
US-10-044-592-96
US-10-044-592-94
US-09-932-161-13
US-09-932-161-13
US-10-044-592-39
US-10-044-592-39
US-10-044-592-41
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Maximum Match 100%
Listing first 45 summaries
                                                                           OM protein - protein search, using sw model
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Maximum DB seq length: 200000000
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Result No.

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PRIOR APPLICATION NUMBER: JP 9-109974
PRIOR FILING DATE: 1997-04-28
PRIOR FILING DATE: SET TYPE: PRI
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Best Local Similarity 100.0
These 31; Conservative
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NAME/KRY: PRPTIDE
LOCATION: (1)..(31)
CTHER INFORMATION: antigen
US-10-044-592-5
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  TITLE OF INVENTION: Therapeutic Compositions and Methods
TITLE OF INVENTION: Relating TO Prolactin Releasing Peptide (FTRP)
FILE REPERENCE: P-UC 354
CURRENT APPLICATION NUMBER: US/10/096,777
CURRENT FILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: US/9/560,915
PRIOR FILING DATE: 2000-04-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Hinuma, Shuji
APPLICANT: Hinuma, Shuji
APPLICANT: Fukusumi, Shoji
TITLE OF INVENTION: Polypeptides, their Production and Use
FILE REPERENCE: 2463US2P
CURRENT APPLICATION NUMBER: US/10/044,592
CURRENT PILING DATE: 2002-01-10
PRIOR APPLICATION NUMBER: PCT/JP98/01923
PRIOR FILING DATE: 1999-25-10
PRIOR FILING DATE: 1999-04-27
PRIOR FILING DATE: 1999-04-27
PRIOR PLING DATE: 1999-04-27
PRIOR PLING DATE: 1997-04-28
NUMBER OF SEQ ID NOS: 96
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Sequence 5, Application US/10044592

PUBLICAND: US20020143152A1

GENERAL INFORMATION:

APPLICANT: Hinnan, Shuji

APPLICANT: Fukusumi, Shoji

TITLE OF INVENTION: Polypeptides, their Production and Use; FILE REPERENCE: 2463US2P

CURRENT APPLICATION NUMBER: US/10/044,592

CURRENT FILING DATE: 2002-01-10
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Best Local Similarity 100.0%; Pred. No. 9.9e-18;
Matches 31; Conservative 0; Mismatches 0;
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                                                                                                                                                              NUMBER OF SEQ ID NOS: 24
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 14
LENGTH: 31
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PRIOR FILING DATE: 1999-25-10
PRIOR APPLICATION NUMBER: PCT/JP98/01923
PRIOR FILING DATE: 1998-04-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4, Application US/10044592
Publication No. US20020143152A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                     ; ORGANISM: Rattus
US-10-096-777-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Murine
US-10-044-592-4
                                                                                                                                                                                                                                                               TYPE: PRT
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Sequence 1, Application US/10044592

Sequence 1, Application US/10044592

GENERAL INFORMATION:
APPLICANT: Hinuma, Shuji
APPLICANT: Hinuma, Shuji
TITLE OF INVENTION: Polypeptides, their Production and Use FILE REFERENCE: 2463US2P
CURRENT APPLICATION NUMBER: US/10/044,592
CURRENT FILING DATE: 2002-01-10
PRIOR FILING DATE: 1999-25-10
PRIOR FILING DATE: 1999-25-10
PRIOR FILING DATE: 1999-427
PRIOR FILING DATE: 1998-04-27
PRIOR PILING DATE: 1998-04-27
                                                                                                                                                                                                                                                                                                                                                                                                    | APPLICANT: Hinuma, Shuji
| APPLICANT: Hinuma, Shuji
| APPLICANT: Fukusumi, Shuji
| TITLE OF INVENTION: Polypeptides, their Production and Use
| TITLE OF INVENTION: Polypeptides, their Production and Use
| FILE REFERENCE: 4563US.P
| CURRENT PILING DATE: 2002-01-10
| PRIOR APPLICATION NUMBER: US 09/403639
| PRIOR APPLICATION NUMBER: US 09/403639
| PRIOR APPLICATION NUMBER: UP 9-109974
| PRIOR APPLICATION NUMBER: UP 9-109974
| PRIOR PILING DATE: 1998-04-27
| PRIOR PILING DATE: 1998-04-27
| RRIOR PILING DATE: 1997-04-28
| NUMBER OF SEQ ID NOS: 96
| SOFTWARE: APPLICATION NUMBER: UP 9-109974
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      Length 31;
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Query Match
100.0%; Score 174; DB 14;
Best Local Similarity 100.0%; Pred. No. 9.9e-18;
Matches 31; Conservative 0; Mismatches 0;
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Length 91;
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APPLICANT: Civelin, Steven

TITLE OF INVENTION: Screening and Therapeutic Methods For TITLE OF INVENTION: Promoting Wakefulness and Sleep;
FILE REPERENCE: Promoting Wakefulness and Sleep;
FILE REPERENCE: Promoting Wakefulness and Sleep;
CURRENT APPLICATION NUMBER: US/09/932,161

PRIOR PILING DATE: 2001-08-17

PRIOR PILING DATE: 2000-04-28

NUMBER OF SEQ ID NOS: 24

SOFTWARE: PRAESEQ for Windows Version 4.0

SEQ ID NO 13

LENGTH: 31
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93.7%; Score 163; DB 9; Length 31;
Best Local Similarity 93.5%; Pred. No. 3.6e-16;
Matches 29; Conservative 0; Mismatches 2; Indels
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1 Similarity 100.0%; Pred. No. 3.1e-17;
31; Conservative 0; Mismatches 0;
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; Sequence 13, Application US/09932161
; Patent No. US20020037533A1
; GENERAL INFORMATION:
  NUMBER OF SEQ ID NOS: 96
SOFTWARE:
SEQ ID NO 94
LENGTH: 91
TYPE: PRT
ORGANISM: Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
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APPLICANT: Hinuma, Shuji
APPLICANT: Pukusumi, Shoji
TITLE OF INVENTION: Polypeptides, their Production and Use
FILE REFERENCE: 2463U32P
CURRENT APPLICATION NUMBER: US/10/044,592
CURRENT PILING DATE: 2002-01-10
PRIOR APPLICATION NUMBER: US/940339
PRIOR PILING DATE: 1999-25-10
PRIOR APPLICATION NUMBER: US/10/P98/01923
PRIOR PILING DATE: 1999-04-27
PRIOR PILING DATE: 1999-04-27
PRIOR PILING DATE: 1999-04-27
PRIOR PILING DATE: 1999-04-27
SPIOR PILING DATE: 1997-04-28
NUMBER OF SEQ ID NOS: 96
                                                                                                                                                                                                                         Length 82;
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Sequence 94, Application US/10044592

Publication Wo. USZ020143152A1

GENERAL INFORMATION:
APPLICANT: Hinuma, Shuji
APPLICANT: Hinuma, Shuji
ITILE OF INVENTION: Polypeptides, their Production and Use
FILE REPERENCE: 2-63-002-01-10

CURRENT APPLICATION NUMBER: US/10/044,592

CURRENT PILING DATE: 1999-25-10

PRIOR APPLICATION NUMBER: BC7/JP98/01923

PRIOR FILING DATE: 1999-25-10

PRIOR FILING DATE: 1999-04-27

PRIOR PILING DATE: 1999-04-27

PRIOR FILING DATE: 1998-04-28
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; LOCATION: (1224)..(1243)
; OTHER INFORMATION: Bracket region depicted in FIG 39.
US-10-044-592-96
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Best Local Similarity 100.0%; Pred. No. 2.8e-17;
Matches 31; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                      1 SRAHOHSMETRIPDINPAWYTGRGIRPVGRF 31
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PRIOR FILING DATE: 1997-04-28
NUMBER OF SEQ ID NOS: 96
SOFTWARE:
SEQ ID NO 1
LENGTH: 82
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                                                                                                                        ; TYPE: PRT
; ORGANISM: Murine
US-10-044-592-1
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FEATURE:
| WANG/KEY: misc_feature |
| LOCATION: (1).-(31) |
| OTHER INFORMATION: primer |
| NAME/KEY: misc_feature |
| LOCATION: (925).-(955) |
| COTHER INFORMATION: primer |
| NAME/KEY: misc_feature |
| LOCATION: (1).-(955) |
| LOCATION: (1).-(955) |
| LOCATION: (1).-(955) |
| COTHER INFORMATION: insert fragment of pmGB3 as depicted in FIG 36 and 37.
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Publication No. US20030171270A1
GENERAL INPORMATION:
APPLICANT: Civelli, Olivier
APPLICANT: Lin, Steven
TITLE OF INVENTION: Therapeutic Compositions and Methods
TITLE OF INVENTION: Relating To Prolactin Releasing Peptide (PrRP)
FILE REFERENCE: P-UC 3534
CURRENT APPLICATION NUMBER: US/10/096,777
CURRENT PILICA DATE: 2002-03-12
PRIOR APPLICATION NUMBER: US/09/560,915
PRIOR PILING DATE: 2000-04-28
NUMBER OF SEQ ID NOS: 24
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Sequence 28, Application US/10044592

Publication No. US20020143152A1

GENERAL INPORMATION:

APPLICANT: Hunma, Shuji

APPLICANT: Hunma, Shuji

TITLE OF INVENTION: Polypeptides, their Production and Use

FILE REFERENCE: 2463U52P

CURRENT APPLICATION NUMBER: US/10/044,592

CURRENT FILING DATE: 2002-01-10

PRIOR PILING DATE: 1999-25-10

PRIOR PILING DATE: 1999-25-10

PRIOR PLING DATE: 1999-04-27

PRIOR PLING DATE: 1999-04-28

NUMBER OF SEQ ID NOS: 96

SOFTWARE:

SEQ ID NO 28

LENGTH: 98
                                                                                                                                                                                                                                                                                                                                    GENERAL INTURCATION:
APPLICANT: HINUME, Shuji
APPLICANT: FURLBUMI, Shuji
APPLICANT: FURLBUMI, Shuji
APPLICANT: FURLBUMI, Shuji
FITIE ROPERINCE: 2463US2P
CURRENT APPLICATION NUMBER: US/10/044,592
CURRENT APPLICATION NUMBER: US/99/403639
PRIOR PILING DATE: 1999-25-10
PRIOR PILING DATE: 1999-25-10
PRIOR PILING DATE: 1999-04-27
PRIOR PILING DATE: 1999-04-28
PRIOR PILING DATE: 1997-04-28
NUMBER OF SEQ ID NOS: 96
SOFTWARE:
SEQ ID NO 41
LENGTH: 33
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                                        93.7%; Score 163; DB 14; Length 32; 93.5%; Pred. No. 3.8e-16;
                                                                                      2; Indels
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                                                                                                                               1 SRAHQHSMETRTPDINPAWYTGRGIRPVGRF 31
                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                              Sequence 41, Application US/10044592 Publication No. US20020143152A1 GENERAL INFORMATION:
                                                                                    29; Conservative
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Best Local Similarity 93.5
Matches 29; Conservative
                                           Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : Bovine
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US-10-044-592-40
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US-10-044-592-41
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                                                                                    Matches
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APPLICANT: Hinuma, Shuji
APPLICANT: Hinuma, Shuji
APPLICANT: Hinuma, Shoji
TITLE OF INVENTION: Polypeptides, their Production and Use
FILE REFERENCE: 2463U82P
CURRENT APPLICATION NUMBER: US/10/044,592
CURRENT APPLICATION NUMBER: US 09/403639
PRIOR PILING DATE: 1999-25-10
PRIOR PILING DATE: 1999-04-27
PRIOR PILING DATE: 1998-04-27
PRIOR APPLICATION NUMBER: DF 9-109974
PRIOR FILING DATE: 1999-04-27
PRIOR FILING DATE: 1999-04-27
NUMBER OF SEQ ID NOS: 96
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APPLICANT: Hinuma, Shuji
APPLICANT: Fukusumi, Shoji
TITLE OF INVENTION: POLYPEPtides, their Production and Use
FILE REFERENCE: 2463052P
CURRENT APPLICATION NUMBER: US/10/044,592
CURRENT FILING DATE: 2002-01-10
PRIOR APPLICATION NUMBER: US 09/403639
PRIOR APPLICATION NUMBER: PCT/JP98/01923
PRIOR FILING DATE: 1999-25-10
PRIOR FILING DATE: 1999-04-27
PRIOR FILING DATE: 1997-04-28
NUMBER OF SEQ ID NOS: 96
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                                                                                                                                                        Length 31;
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Best Local Similarity 93.5%; Pred. No. 3.6e-16;
Matches 29; Conservative 0; Mismatches 2;
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Pred. No. 3.6e-16;
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SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 13
                                                                                                                                                                                                                                                                                                                                                                                             Sequence 39, Application US/10044592; Publication No. US20020143152A1; GENERAL INFORMATION:
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Publication No. US20020143152A1
GENERAL INFORMATION:
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93.5%;
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Best Local Similarity 93.59
                                                               TYPE: PRT
ORGANISM: Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Bovine
US-10-044-592-39
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ORGANISM: Bovine
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US-10-044-592-39
                                                                                                          US-10-096-777-13
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SEQ ID NO 40
LENGTH: 32
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Gaps

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RESULT 15
US-10-044-592-38

i Sequence 38, Application US/10044592

publication No. US20020143152A1

GENERAL INFORMATION:

APPLICANT: Hinuma, Shuji

TITLE OF INVENTION: Polypeptides, their Production and Use

FILE REFERENCE: 2463U52B

CURRENT APPLICATION NUMBER: US/10/044,592

CURRENT PILING DATE: 2002-01-10

PRIOR PPLING DATE: 1999-25-10

PRIOR PILING DATE: 1999-25-10

PRIOR PILING DATE: 1999-25-10

PRIOR PILING DATE: 1999-64-27

PRIOR PILING DATE: 1999-04-28

NUMBER OF SEQ ID NOS: 96

SOFTWARE:

SEQ ID NO 38

IENOTH: 98

TYPE: PRI

YORGANISM: Bovine

US-10-044-592-38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 93.7%; Score 163; DB 14; Length 98; Best Local Similarity 93.5%; Pred. No. 1.2e-15; Matches 29; Conservative 0; Mismatches 2; Indels
                       1 SRAHQHSMETRIPDINPAWYTGRGIRPVGRF 31
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Search completed: December 3, 2003, 19:17:37 Job time : 22.5 secs

us-09-868-885b-18.xpx

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Query Match
Best Local Similarity
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                                                                                                                                                                                           December 3, 2003, 19:05:30 ; Search time 10.5 Seconds (without alignments) 283.927 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                     1 SRAHQHSMETRTPDINPAWYTGRGIRPVGRF 31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        283308 segs, 96168682 residues
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                                                                                                                                OM protein - protein search, using sw model
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T2
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Gapop 10.0 , Gapext 0.5
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AH2762
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Listing first 45 su
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174
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Maximum DB seq length: 200000000
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Match Length DB
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1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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Perfect score:
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No.
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probable transport hypothetical 41.1K hypothetical prote probable glutathio hypothetical prote proteporphyrin IX excinuclease ABC c protoporphyrin IX protoporphyrin IX protoporphyrin IX protoporphyrin IX	ALIGNMENTS	PRESULT 1 JC7607 prolactin-releasing peptide - rat C)Species: Rattus norvedicus (Norway rat) C;Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 30-Jun-2001 C;Accession: JC7607 R;Yamada, M.; Ozawa, A.; Ishii, S.; Shibusawa, N.; Hashida, T.; Ishizuka, T.; Hosoya, T. R;Yamada, M.; Ozawa, A.; Ishii, S.; Shibusawa, N.; Hashida, T.; Ishizuka, T.; Hosoya, T. R;Yamada, M.; Ozawa, A.; Ishii, S.; Shibusawa, N.; Hashida, T.; Ishizuka, T.; Hosoya, T. R;Yamada, M.; Ozawa, A.; Ishii, S.; Shibusawa, N.; Hashida, T.; Ishizuka, T.; Hosoya, T. A;Title: Isolation and characterization of the rat prolactin-releasing peptide gene: Mu. A;Reference number: JC7607; MUID:21092785; PMID:11178959 A;Accession: JC7607 A;Molecule type: DNA A;Accession: JC3607 A;Molecule type: DNA A;Accession: JC3607 A;Accession:	Score 174; DB 2; Length 83; Pred. No. 4.4e-18; ; Mismatches 0; Indels 0; Gaps 0; rGRGIRPVGRF 31	RESULT 2 T50904 Mg protoporphyrin methyl transferase [imported] - Rubrivivax gelatinosus C;Species: Rubrivivax gelatinosus C;Species: Rubrivivax gelatinosus C;Species: Rubrivivax gelatinosus C;Accession: T50904 R;Nagashima, K.V.; Igarashi, N.; Harada, J.; Nagashima, S.; Matsuura, K.; Shimada, K. submitted to the RMID Data Library, November 1999 A;Description: Determination of Nucleotide Sequences of Rubrivivax gelatinosus Photosyn A;Reference number: Z55270 A;Accession: T50904 A;Ratus: preliminary; translated from GB/EMBL/DDBJ A;Rolecule type: DNA A;Residues: 1-1236 <nag> A;Cross-references: EMBL:AB034704; PIDN:BAA94057.1 A;Ross-references: EMBL:AB034704; PIDN:BAA94057.1 A;Ross-references: EMBL:AB034704; PIDN:BAA94057.1 A;Ross-references: BMBL:AB034704; PIDN:BAA94057.1 A;Ross-references: BMBL:AB034704; PIDN:BAA94057.1 A;Ross-references: BMBL:AB034704; PIDN:BAA94057.1 A;Ross-references: BMBL:AB034704; PIDN:BAA94057.1 A;Genetios: C;Genetios:</nag>	61; DB 2; Length 1236; No. 1.9;
F86019 S47704 C836955 C836955 C836959 A87664 T46550 D87570 D87570 S77349 T56031 T56031 T56031 T56031 S75000 S75000	ALIG	rway rat rision 3 3.; Shib 11, 53-5 121, 53-5 12109278 2; DDBJ: arachido secreti	8 4 5 E E	rase [im s vision 2 Harada, ry, Nove Nucleoti d from G d; PIDN:	Score Pred.
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0 11 24 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4		RESULT 1 JC7607 prolactin-releasing C;Species: Rattus nc C;Date: 30-Jun-2001 C;Accession: JC7607 R;Yamada, M.; Ozawa, Biochem. Blophys. Re A;Title: Isolation a A;Reference number: A;Contents: Spleen A;Accession: JC7607 A;Molecule type: DW A;Residues: 1-83 *YZ A;Cross-references: C;Comment: This pept C;Genetics: C;Genetics: A;Gnetics: A;Gnetics: A;Gnetics: A;Harrons: 33/1	Query Match Best Local Matches 3 Qy 1 Db 22	RESULT 2 T50904 Mg protoporpl C; Species: R C; Date: 21-0 C; Date: 21-0 C; Accession: R; Nagashima, submitted to A; Reference A; Recension: A; Ratues: pr A; Ratues: pr A; Residues: C; Genetics: A; Gross-refe A; Gross-refe A; Gross-refe C; Genetics: C; Superfamil	Query Match Best Local

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hypothetical protein all1686 [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C;Accession: AH2016
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguc? Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium AA;Reference number: AB1807; MUID:21595285; PMID:11759840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A,Gene: PA4601
C,Superfamily: oxygen sensor with signal transduction diguanylate cyclase and c-di-GMP
                                                                                       Cispecies: Rattus norvegicus (Norway rat)
Cispecies: Rattus norvegicus (Norway rat)
Cipate: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 05-Nov-1999
Cipate: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 05-Nov-1999
Cipate: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 05-Nov-1999
Cipate: Characterization of unr; A. Bellicer, A. Rijeterence number: $11210; MUID:99370473; PMID:2204029
A.Reference number: $11210
A.Reference number: $11210
A.Molecule type: mRNA
A.Residues: 1-798 - CJEF-
A.Residues: 1-798 - CJEF-
Circoss-references: EMBL:X52311; NID:957454; PIDN:CAA36549.1; PID:957455
Circoss-references: DNA binding
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Pred. No. 17;
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Pred. No. 32;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5; Mismatches
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Matches 10; Conserv
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A;Molecule type: DNA
A;Residues: 1-303 <KUR>
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N;Contains: excision endonuclease ABC (BC 3.1.-.-) chain A
N;Contains: excision endonuclease ABC (BC 3.1.-.-) chain A
C;Species: Methanobacterium thermoautotrophicum
C;Species: Methanobacterium thermoautotrophicum
C;Accession: H69157
R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
R;Smith, D.R.; Doucette-Stamm, L.A.; Mang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.
Ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Cross-references: GB:AE000828; GB:AE000666; NID:g2621504; PIDN:AAB84949.1; PID:g26215d
A,Experimental source: strain Delta H
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                                                                                                                                                                                                                             probable magnesium chelatase (EC 4.99.1.-) chain H BchH - Heliobacillus mobilis
C;Species: Heliobacillus mobilis
C;Species: Heliobacillus mobilis
C;Date: 02-5ep-2000 #sequence_revision 02-Sep-2000 #text_change 15-Sep-2000
C;Accession: T31462
R;Xiong, J.; Inoue, K.; Bauer, C.B.
R;Xiong, J.; Inoue, K.; Bauer, C.B.
R;Xiong, J.; Inoue, K.; Bauer, C.B.
A;Title: Tracking molecular evolution of photosynthesis by characterization of a major )
A;Reference number: Z21036; MUID:99061957; PMID:9843979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Gene: MTH443
A;Start codon: TTG
C;Superfamily: excinuclease ABC chain A; ATP-binding cassette homology
C;Reywords: ATP; DNA binding; DNA repair; duplication; hydrolase; nucleotide binding;
F;38-45/Region: nucleotide-binding motif A (P-loop)
F;632-915/Domain: ATP-binding cassette homology <ABCE>
F;649-656/Region: nucleotide-binding motif A (P-loop)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Gene: bchH
C;Superfamily: Rhodobacter capsulatus magnesium-protoporphyrin O-methyltransferase
C;Keywords: lyase
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1292 <XIO>
A;Coss-references: EMBL:AF080002; NID:g3820536; PID:g3820560; PIDN:AAC84033.1
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Reference number: A69000; MUID:98037514; PMID:9371463
A;Accession: H69157
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
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Pred. No. 5.5;
3; Mismatches 6; Indel8
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Pred. No. 7.8;
0; Mismatches 4; Indels
IndelB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----RGIRPVGRF 31
8
                                                                                     3 AHQHSMETRIPDINPAWYTG-----RGIRPV 28
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1176 ETRIKTLNPKWYEGMLKHGYEGVREI 1201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9 ETRTPDINPAWYTG-----RGIRPV 28
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9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       uvery Match 33.3%;
Best Local Similarity 42.3%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 42.1%;
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  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-962 <MTH>
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12;
  Matches
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30.2%;

Conservative

Query Match Best Local Similarity (

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A; Gene: all1686

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RibelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, J. Mazur, M.; Goltsman, B.; Selkov, B.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letes Proc. Natl. Acad. Sci. US.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella meliten A;Reference number: AD3252; PMID:11756688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Reaidues: 1-972 <COL>
A;Cross-references: GB:285982; GB:AL123456; NID:g3261718; PIDN:CAB06633.1; PID:g1838989
A;Experimental source: strain H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     genome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Holroyd,
                                                                                                                                                                                                                                                                                                                                          N;Alternate names: uvrA protein
N;Contains: excision endonuclease ABC (BC 3.1...) chain A
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 02-Feb-2001
C;Accession: A70619
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Go.; Connor, R.; Deviin, K.; Feltwell, T.; Gentles, S.; Hamilin, N.; Holr, Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A;Authors: Squares, R.; Sullston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Tile: Deciphering the biology of Mycobacterium tuberculosis from the complete; A;Recession: A70619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Superfamily: excinuclease ABC chain A; ATP-binding cassette homology C;Reywords: ATP, DNA binding; DNA repair; hydrolase; nucleotide binding; P-loop P;32-39/Region: nucleotide-binding motif A (P-loop) P;637-920/Domain: ATP-binding cassette homology <ABCE> P;654-661/Region: nucleotide-binding motif A (P-loop)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 excinuclease ABC chain A BME10878 [imported] - Brucella melitensis (strain 16M) C;Species: Brucella melitensis C;Date: 01-Peb-2002 #sequence_revision 01-Peb-2002 #text_change 15-Peb-2002 C;Accession: AH3361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                        Gaps
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                                                                                                                                                                                                                                                                                                                                excinuclease ABC chain A - Mycobacterium tuberculosis (strain H37RV)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Length 972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Indels
                                 4; Indels
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                                                                                                ----RGIRPVGRF 31
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                                                                                                                                            29.9%; Score 52; DB 39.5%; Pred. No. 30; ive 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Mismatches
      Pred. No. 30;
1; Mismatches
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      39.54;
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Best Local Similarity 39.5-
Best Local Similarity 139.5-
Conservative
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   Best Local Similarity 39.5
Matches 15; Conservative
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                                                                                                11 RIPDINPAWYIG-
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A,Molecule type: DNA
A,Residues: 1-974 <KUR>
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C;Species: Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 10-May-2001
C;Accession: B87083
R;Cole, S.T.; Esglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Hq
R; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd,
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AyAthoras Rutter, S.; Seeger, K.; Simon, S.; Simmonde, M.; Skelton, J.; Squaree, R.; Sq
A;Title: Massive gene decay in the leprosy bacillus.
A;Reference number: A86909; MUID:21128732; PMID:11234002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:AE004127; GB:AE003852; NID:g9654808; PIDN:AAF93567.1; GSPDB:GN001
A;Experimental source: serogroup O1; strain N16961; biotype Bl Tor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RiHeidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, B. J., R.R.; Makalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       excinuclease ABC chain A [similarity] - Vibrio cholerae (strain N16961 serogroup N;Contains: excision endonuclease ABC (EC 3.1.-.-) chain A C;Species: Vibrio. cholerae C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 24-Aug-2001 C;Accession: Ag2229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Superfamily: excinuclease ABC chain A; ATP-binding cassette homology C;Reywords: AFF; DNA binding; DNA repair; hydrolase; nucleotide binding; P-loop F;31-38/Region: nucleotide-binding motif A (P-loop) F;639-646/Region: nucleotide-binding motif A (P-loop)
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A;Cross-references: GB:BA000019; PIDN:BAB78052.1; PID:g17135506; GSPDB:GN00179
A;Experimental source: strain PCC 7120
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                                                                                                                                                                   Length 303;
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                                                                                                                                                                                                                                                                                                                                          Score 52.5; DI
Pred. No. 7.2;
2; Mismatches
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Query Match Best Local Similarity 39.5-Local 15, Conservative

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A; Residues: 1-940 <HEI>

A; Map position: 1

A; Gene: VC0394

Genetics:

A;Status: preliminary A;Molecule type: DNA

A; Accession: A82329

29.9%; Score 52;

Query Match

A; Molecule type: DNA A; Residues: 1-969 <STO> A;Status: preliminary

C, Genetica:

A; Accession: B87083

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A) Status incless and sequence not shown; translation not shown
A) A) Residues: 1-943 < TIGR>
A) Residues: 1-943 < TIGR>
A) Residues: 1-943 < TIGR>
A) Accross = references: 8train Rd KW20
B) dea 177, 23-28, 1996
Gene 177, 23-28, 1996
Gene 177, 23-28, 1996
A) Accession: JC5157; MUID:97080495; PMID:8921840
A) Accession: JC5157
A) Accession: JC51
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AjGene: uvra

Cjrunction:

AjPescription: has ATPase and DNA binding activity; involved in DNA repair

AjPescription: has ATPase and BC chain A; ATP-binding cassette homology

Cjruperfamily: excinuclease ABC chain A; ATP-binding cassette homology

Cjrupersors: ATP; DNA binding; DNA repair; duplication; hydrolase; nucleotide binding; I

F;31-38/Region: nucleotide-binding motif A (P-loop)

F;640-647/Region: nucleotide-binding motif A (P-loop)
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A;Molecule type: DNA
A;Residues: 1-176 <JAU>
A;Cross-references: EMBL:275161; NID:91420572; PID:e252411; PID:91420573; GSPDB:GN0001:
A;Experimental source: strain S288C
                                                                                                                                                                                   NiAlternate names: uvrA protein
NiContains: excision endonuclease ABC (EC 3.1.-.-) chain A
Cippedies: Haemophilus influenzae
Cippedies: Haemophilus influenzae
Cipate: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 02-Feb-2001
CiAccession: D64057; JC5157
RiPelschmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, B.F.; Kerlavage, RiPielschmann, R.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kirkness, B.F.; Kerlavage, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M. Science 269, 496-512, 1995
A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd. A;Reference number: A64000; MuID:95350630; PMID:7542800
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N;Alternate names: hypothetical protein 05315
C;Species: Saccharomyces cerevisiae
C;Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 19-Apr-2002
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Pred. No. 7.8;
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A;Map position: 15R
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A,Residues: 1-503 <HEL>
A,Cross-references: GB:AE004228, GB:AE003852; NID:g9655997; PIDN:AAF94657.1, GSPDB:GN001
A,Experimental source: serogroup 01, strain N16961; biotype El Tor
                                                                                                                                                                                                                                             A82193
Sun/mucleolar protein family protein VC1502 [imported] - Vibrio cholerae (strain N16961
                                                                                                                                                                                                                                                                                                                                      C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C;Accession: A8219;
R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J. chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, I. R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
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A; Accession: T21075
A; Molecule type: DNA
A; Redidues: L-294 «MLL»
A; Cossereferences: EMEL: Z50873; PIDN: CAA90762.1; GSPDB: GN00028; CESP: F19H6.1
A; Experimental source: clone F17E5
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A;Cross-references: EMBL:Z68115; PIDN:CAA92169.1; GSPDB:GN00028; CESP:F19H6.1
A;Experimental source: clone F19H6
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hypothetical protein F19H6.1 - Caenorhabditis elegans

c;Species: Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 115-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 17-Mar-2000

C;Accession: T21075; T21124

R;McMurray, A.

R;McMurray, A.
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A,Introns: 55/3; 85/2; 113/3; 150/1; 192/3; 266/2
C,Superfamily: kinase-related transforming protein; protein kinase
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44.8%; Pred. No. 11;
1ve 2; Mismatches 12; Indels
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les 11; Conserv
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A; Status: preliminary
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A;Gene: VC1502
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NER3_HUMAN
UVRA_HAEIN
UVRA_HAEIN
UVRA_FSS_BUCAI
R167_ECOL6
UVRA_ECOL6
UVRA_SALLT
UVRA_SALLT
UVRA_SALLT
UVRA_RICCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRRP RAT
PRRP BOVIN
NERP HUMAN
NER3 BOVIN
UVRA METTH
UVRA RAT
UVRA MYCLE
UVRA MYCLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    UVRA_SYNY3
UVRA_STRCO
BCHH_RHOSH
                                                                                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RHILO
                                                               OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CYSC_YERPE
                                                                                                                                                                                                                                     Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             UVRA UVRA
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length: 2000000000
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174
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Match Length
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No.
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        34
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        27.6
        569
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        UVRA VITST
        Q08518 vitreoscill

        36
        48
        27.6
        719
        1
        NRPI_YEAST
        P32770 saccharomyc

        36
        48
        27.6
        798
        1
        UNR HUMAN
        O7534 home sapien

        39
        48
        27.6
        949
        1
        UVRA_NEIMS
        Q9just neisseria m

        40
        48
        27.6
        949
        1
        UVRA_NEIGO
        O5968 neisseria g

        41
        48
        27.6
        950
        1
        UVRA_TREPA
        O9357 treponema p

        41
        48
        27.6
        1087
        1
        XPO7_HUMAN
        Q9uias home saplen

        42
        1087
        1
        XPO7_HUMAN
        Q9uias home saplen

        43
        48
        27.6
        1087
        1
        XPO7_HUMAN
        P30567 mus musculu

        44
        47.5
        27.3
        501
        1
        TRA2_MOUSE
        P26162 rhodobacter

        45
        47.5
        27.3
        941
        1
        GCMS_MOUSE
        P39429 mus musculu
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ALIGNMENTS

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PRE PART

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MOD RES
SEQUENCE
                        MOD RES
SEQUENCE
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                    TPDINPAWYTGRGIRPVGRFGRRRATPRDVTGLGQLSCLPL
DGRTKFSQRG -> SECLTYGKQPLTSFHPFTSQMPP (in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -i. FUNCTION: Stimulates prolactin (PRL) release and regulates the expression of prolactin through its receptor GPR10. May stimulate lactotrophs directly to secrete PRL.
-i. TISSUE SPECIFICITY: MEDULA OBLONGARA AND HYPOTHALAMUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2003 (Rel. 41, Last annotation update)
Prolactin-releasing peptide precursor (PrRP) (Prolactin-releasing hormone) (Contains: Prolactin-releasing peptide PrRP31; Prolactin-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidae, Bovinae, Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUB=Brain;
MEDLINE=B8268781; PubMed=9607765;
Hinnma S., Habata Y., Fujii R., Kawamata Y., Hosoya M., Fukusumi Kitada C., Masuo Y., Asano T., Matsumoto H., Sekiguchi M., Kitada C., Masuo Y., Asano T., Matsumoto H., Sekiguchi M., Kitada T., Nishimura O., Onda H., Fujino M.;
"A prolactin-releasing peptide in the brain.";
Nature 393:272-276(1998).
                                                                                                                                                                                                                                                                                                               AMIDATION (G-53 PROVIDE AMIDE GROUP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRRP31.
PRRP20.
                                                                                                                                                                                                                                             PROLACTIN-RELEASING PEPTIDE PRRP31.
PROLACTIN-RELEASING PEPTIDE PRRP20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AB015417; BAA29025.1; -.
Hormone; Amidation; Signal; Cleavage on pair of basic residues.
                                                                                                            EMBL; AB015418; BAA29026.1; -.
EMBL; AF521930; AAM82154.1; -.
PIR; JC7607; ZO7607; ZO7607; APPLE; JC7607; APPLE; JC7607; Signal; Cleavage on pair of basic residues;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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Pred. No. 1.1e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROLACTIN-RELEASING PEPTIDE PROLACTIN-RELEASING PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IndelB
                                                                                                                                                                                                                                                                                                                                                                                                                     DOC75A264EER4F29 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98 A.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22 SRAHQHSMETRTPDINPAWYTGRGIRPVGRF 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 SRAHQHSMETRIPDINPAWYTGRGIRPVGRF 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A., AND SEQUENCE OF 23-52
                                                                                                                                                                                                                                                                                                                                                                               isoform 2). /PTId=VSP_0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                          83 AA; 9215 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  releasing peptide PrRP20]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                Alternative splicing.
21
SIGNAL
1 21
PEPTIDE 22
PEPTIDE 33
PROPEP 57
MOD RES 52
VARSPLIC 33
83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRRP BOVIN P81264;
                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRPTIDE
PEPTIDE
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10 PRRP B B126

PRATE B B126

DT 30-MAY-

DT 30-MAY-

DT 30-MAY-

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-1- TISSUR SPRCIPICITY: MEDULIA OBLONGATA AND HYPOTHALAMUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=99426652; PubMed=10498338; Pujil R., Fukusumi S., Hosoya M., Kawamata Y., Habata Y., Hinuma S., Sekiguchi M., Kitada C., Kurokawa T., Nishimura O., Onda H., Sumino Y., Pujino M., "Ilasue distribution of prolactin-releasing peptide (PrRP) and its
                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hinuma S., Habata Y., Fujii R., Kawamata Y., Hosoya M., Fukusumi S., Kiteda C., Masuo Y., Asano T., Matsumoto H., Sekiguchi M., Kurokawa T., Nishimura O., Onda H., Fujino M.; *A prolactin-releasing peptide in the brain.";
AMIDATION (G-54 PROVIDE AMIDE GROUP). 08AC35A13B0FA908 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                               30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
38-FEB-2003 (Rel. 41, Last annotation update)
Prolactin-releasing peptide precursor (PRRP) (Prolactin-releasing hopmone) (Contains: Prolactin-releasing peptide precursor (PRRP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AMIDATION (G-54 PROVIDE AMIDE GROUP)
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                                                                               Score 163; DB 1; Length 98;
Pred. No. 5.4e-17;
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Pred. No. 5.3e-15;
1; Mismatches 4;
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                                                                                                        Pred. No. 5.4e
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                  87
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                                                                                                                                                                                                                                             23 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Brain; MEDLINE=98268781; PubMed=9607765;
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                               10544 MW;
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83.9%;
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                                                                                                        llarity 93.5%;
Conservative
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                                                                                 93.78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            releasing peptide PrRP20]
                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature 393:272-276(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sapiens (Human)
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hes 26; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE SPECIFICITY
                                                                                                           Local Similarity
tes 29, Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SECUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             87 AA;
                               98 AA;
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ID PRRP HUMAN
AC P81277;
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195 RARPHSLMIYSDDLGATWHHGRLIKPM 221
2 RAHQHSMETRIPDINPAWYTGRGIRPV 28
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ZN_PING
                                                                             RESULT 5
UVRA_METTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation her Buropaen Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                          (Rel. 41, Last sequence update)
(Rel. 41, Last annotation update)
(EC 3.2.1.18) (Membrane sialidase) (Ganglioside sialidase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  glycoconjugates.
--- CATALNITY: Hydrolygis of alpha-(2->3)-, alpha-(2->6)-, alpha-(2->8)-glycosidic linkages of terminal sialic residues in oligosaccharides, glycoproteins, glycolipids, colominic acid and synthetic substrates.
--- SUBCELLIARA LOCATION: Membrane-associated (By similarity).
--- TISSUB SPECIFICITY: Expressed in brain.
--- SIMILARITY: BELONGS TO FAMILY 33 OF GLYCOSYL HYDROLASES.
                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-59143165; PubMed=9988745; Miyaqi T., Wada T., Iwamateu A., Hata K., Yoshikawa Y., Tokuyama S., Swada M.; Wada T., Iwamateu A., Hata K., Yoshikawa Y., Tokuyama S., Swada M.; Choning and characterization of a plasma membraneassociated sialidase specific for gangliosides."; J. Blol. Chem. 274:5004-5011(1999).

-i- FUNCTION: Plays a role in modulating the ganglioside content of the lipid bilayer at the level of membrane-bound sialyl
                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A., PARTIAL SEQUENCE, AND CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32.2%; Score 56; DB 1; Length 428;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    418B34F3245A8F21 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Potential.
By similarity.
Potential.
               31
                              23 SRTHRHSMBIRTPDINPAWYASRGIRPVGRF 53
                                                                                                                            428 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BNR 1.
BNR 2.
BNR 3.
FRIP MOTIF.
By similarity.
Potential.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF02012; BNR; 3.
Hydrolase; Glycosidase; Membrane; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Potential.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Potential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Potential
                                                                                                                                                                                                                         (N-acetyl-alpha-neuraminidase 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AB008184; BAA75071.1; -.
InterPro; IPR002860; GH_BNR.
                                                                                                                                                       28-FEB-2003 (Rel. 41, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  47916 MW;
                                                                                                                           STANDARD:
                                                                                                                                                                                                                                                       taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  428 AA;
                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9913;
                                                                                                                       NER3 BOVIN
097859;
                                                                                                                                                                                                          Sialidase 3
                                                                                                                                                                        28-FEB-2003
                                                                                                                                                                                           28-PEB-2003
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SITE
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                                                                                                                                                                                                                                                                                                   A Smith D.R., Dougette-Stamm L.A., Deloughery C., Lee H.-M., Dubois J., Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K., Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Olu D., A Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R., Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S., A McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M., A Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N., Tomplete genome sequence of Methanobacterium thermoautotrophicum deltam: functional analysis and comparative genomics.";

T. Becteriol. 179:7135-7155(1997).

- I- FUNCTION: The UvxBC repair system catalyzes the recognition and processing of DNA lesions. UvxA is an ATPase and a DNA-binding current analyses and analyses composed of 2 uvxA and 2 uvxB subunite scans DNA for abnormalities. When the presence of a lesion has been verified by uvxB, the uvxA molecules dissociate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -1- SUBCELLUIAR LOCATION: Cytoplasmic (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TIGRPAMS; TIGRO0630; uvra; 1.
PROSITE; PS10021; ABC TRANSPORTER 1; 2.
PROSITE; PS1093; ABC_TRANSPORTER 2; 2.
SOS response; Excision nuclease; DNA repair; DNA recombination;
DNA excision; ATP-binding; DNA-binding; Repeat; Zinc; Metal-binding;
                                                                                                   UvrABC system protein A (UvrA protein) (Excinuclease ABC subunit A) UVRA OR MTH443.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (By similarity).

SUBUNIT: Forms a heterotetramer with uvrB during the search for lesions (By similarity).
                                                                                                                                                          Archaea, Buryarchaeota, Methanobacteria, Methanobacteriales,
Methanobacteriaceae, Methanothermobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 962;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              38 45 ATP (POTENTIAL).
649 656 ATP (POTENTIAL).
7.14 C4-TYBE.
962 AA; 108395 MW; 2COEF?FC41CCD060 CRC64;
                                   30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
28-FKB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 56;
Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam, PF00005, ABC tran; 2.
ProDom; PD000006; ABC transporter; 1.
SMART; SM00382; AAA; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HAMAP, MP_00205; -; 1.
InterPro; IPR003593; AAA ATPase.
InterPro; IPR003493; ABC_transporter.
InterPro; IPR004602; UvrF.
                                                                                                                                         Methanobacterium thermoautotrophicum.
                                                                                                                                                                                                                                                                 STRAIN=Delta H;
MEDLINE=98037514; PubMed=9371463;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AE000828; AAB84949.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zinc-finger; Complete proteome.
NP_BIND 38 45 A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32.2%;
STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; H69157; H69157.
                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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Best Local Similarity
                                                                                                                                                                                                      NCBI_TaxID=187420;
  UVRA METTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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Gaps

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11; Indels

Pred. No. 1.2; 6; Mismatches

37.0%;

Local Similarity

Best Loca Matches

Conservative

Matches

g

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                                                                                                                                                                                                   MEDLINE-EI Tor Nic961 / Serctype 01;
MEDLINE-20406833; PubMed=10952301;
Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
Dodson R.J., Haft D.H., Hickey B.K., Peterson J.D., Umayam L.A.,
Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
McDonald L., Utterback T., Pleischmann R.D., Nierman W.C., White O.,
Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (By similarity).
--- SUBUNIT: Forms a heterotetramer with uvrB during the search for lesions (By similarity).
--- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
---- SUBCELLULAR LOCATION: CYTOPLASPORTER FAMILY. UVRA SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                              -i- FUNCTION: The UNTABC repair system catalyzes the recognition and processing of DNA lesions. UNTA is an ATRase and a DNA-binding protein. A damage recognition complex composed of 2 untA and 2 uvrB subunits scans DNA for abnormalities. When the presence of lesion has been verified by uvrB, the uvrA molecules dissociate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PP00005; ABC tran; 2.
ProDom; PD000006; ĀBC transporter; 1.
TIGRPAMs; TIGR0630; uvra; 1.
PROSITE; PS0021; ABC TRANSPORTER 1; 2.
SNOS TESPONBE; EXCISION INCLEASE; DNA repair; DNA recombination;
DNA excision; ATP-binding; DNA-binding; Repeat; Zinc; Metal-binding;
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
UVRABC system protein A (UVrA protein) (Excinuclease ABC subunit A)
UVRA OR VC0394.
                                                                                                                                                                                                                                                                                                                                                                                       "DNA sequence of both chromosomes of the cholera pathogen Vibrio
                                                                                                           Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales; Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 52; DB 1; Length 940; Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           739 765 C4-TYPE.
940 AA; 104327 MW; 84F93B9DF686F6F2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11 RIPDINPAWYTG------RGIRPVGRF 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4;
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ATP (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATP (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HAMAP; MF 00205; -; 1.
InterPro; IPR003439; ABC transporter.
InterPro; IPR004602; UvrĀ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zinc-finger, Complete proteome.
NP BIND 31 38 ATI
ZN_FING 252 279 C4
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39.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 406:477-483(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      279
646
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es 15; Conserv
                                                                                                                                                                                          FROM N.A
                                                                                             Vibrio cholerae
                                                                                                                                                      NCBI_TaxID=666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 8
UVRA_MYCLE
ID UVRA_MYCLE
                                                                                                                                                                                                                                                                                                                                                                                                          cholerae.";
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ZN_FING
SEQUENCE
                                                                                                                                                                                        SEQUENCE
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Matches
                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the Buropean Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae, Rattus.
                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                    18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Jeffers M., Paciucci R., Pellicer A.,
"Characterization of unr, a gene closely linked to N-ras.";
Nucleic Acids Res. 18:4891-4899(1990).
-i- PUNCTION: RNA-BINDING PROTEIN (BY SIMILARITY).
-i- SUBCELULIAR LOCATION: Cytoplasmic.
-i- SIMILARITY: BELONGS TO THE COLD-SHOCK DOMAIN (CSD) FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30.5%; Score 53; DB 1; Length 798; 43.5%; Pred. No. 6.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8; Indels
                  4; Indels
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                                                                                 11 RIPDINPAWYIG------RGIRPVGRF 31
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CSD 2 (INCOMPLETE).
CSD 3.
CSD 5.
CSD 6.
CSD 6.
CSD 6.
CSD 7.
CSD 7.
CSD 8.
CSD 9.
                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
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                                                                                                                                                                                            798 AA
                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 6.4, 5; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Testis; Pubmed=2204029; MEDLINE=90370473; Pubmed=2204029;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSSP, PIS277; 1MJC.
InterPro; IRR002059; Cold_shock.
Jefam; PP00313; CSD; 7.
ProDom; PD000621; Cold_shock; 1.
SMART; SM00357; CSP; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00352; COLD_SHOCK; 4.
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UVRA_VIBCH

ID UVRA_VIBCH

STANDARD;

1

Q9KUM5;

DT 28-FEB-2003 (Rel. 41, Created)
                                                                                                                                                                                                                                 Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               88894 MW;
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10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X52311; CAA36549.1; -. PIR; S11210; S11210.
                    16; Conservative
                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                              Rattus norvegicus (Rat)
                                                                                                                                                                                                                               01-NOV-1990 (Rel. 16,
01-NOV-1990 (Rel. 16,
16-OCT-2001 (Rel. 40,
UNR protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RNA-binding, Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             798 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
SEQUENCE
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                                                                                                                                                                                        UNR RAT
P18395;
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RESULT 6

IUNR RAT

AC P183

DT 16-00

DE UNR OS RATE.

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||| ||| ||| ||| 694 RIPRSNPATYTGIFTPIRELFAGTQESRSRGYQP-GRF 730
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2

Gaps

18;

Indels

Matches

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Best

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JVRA_MYCTU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                MEDIATE 21128732; PubMed=11234002;

MEDIATE 21128732; PubMed=11234002;

Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R.,

Moeeler P.R., Honore N., Garnier T., Churcher C., Harris D.,

Mungall K., Basham D., Brown D., Chillingworth T., Connor R.,

Mungall K., Deviln K., Duthoy S., Feltwell T., Fraser A., Hamlin N.,

Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,

Murphy L., Oliver K., Quail M.A., Simon S., Steptwell T., Reason J., Squares R.,

A guares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,

A guares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,

Barrell B.G.;

"Massive gene decay in the leprosy bacillus.";

"A connor M. Massive gene decay in the leprosy bacillus.";

"A connor M. Massive gene decay in the leprosy bacillus.";

"A connor M. Massive gene decay in the leprosy bacillus.";

"A connor M. Massive gene decay in the leprosy bacillus.";

"A connor M. Massive gene decay in the leprosy bacillus.";

"A connor M. Massive gene decay in the leprosy bacillus.";

"A connor M. Massive gene decay in the leprosy bacillus.";

"I mature 409:1007-1011(2001).

"I processing of DNA lessons Unva A is an ATPase and a DNA-binding protein. A damage recognition complex composed of 2 uvra and 2 uvra molecules dissociate for the massive denotation when the presence of a connormal mature and a protein when the presence of a connormal mature when the prese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (By similarity).

SUBUNIT: Forms a heterotetramer with uvrB during the search for lesions (By similarity).

SUBCELLUIA LOCATION: Cytoplasmic (By similarity).

SUBCELLUIAR LOCATION: Cytoplasmic (By similarity).

SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Probom; PD000006; ABC transporter; 1.
TIGRFAMS; TIGR00630; uvra; 1.
PROSITE; PS00211; ABC TRANSPORTER 1; 2.
PROSITE; PS50893; ABC TRANSPORTER 2; 1.
SOS response; Excision nuclease; DNA repair; DNA recombination;
DNA excision, ATP-binding; DNA-binding; Repeat; Zinc; Metal-binding;
Zinc-finger; Complete proteome.
     28-FEB-2003 (Rel. 41, Last sequence update)
UVrABC system protein A (UvrA protein) (Excinuclease ABC subunit A).
Wycobacterium leprae.
Bacteria. **L.**
                                                                                                                                                                                 Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Corynebacterineae, Mycobacteriaceae, Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 52; DB 1; Length 969;
Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        106377 MW; 6668141833C53DB5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATP (POTENTIAL).
C4-TYPE.
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Leproma; ML1392; --: 1.

HAMAP; MF 00205; -; 1.

InterPro; IPR003439; ABC transporter.

InterPro; IPR004602; Uvrā.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C4-TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AL583921; CAC31773.1; -.
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39.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32
258
652
652
651
751
751
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Best Local Similarity
                                                                                                                                                                                                                                                                 [1] SEQUENCE FROM N.A.
                                                                                                                                                                                                                                NCBI TaxID=1769;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NP_BIND
ZN_FING
SEQUENCE
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ZN FING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Peterson J., Desboy R., Dodson R., Gwinn M.L., Haft D., Hickey B.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Harris D.
                                                                                                                                                                                                                                                                                                                                                              s:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: The UVABC repair system catalyzes the recognition and processing of DNA lesions. UvrA is an ATPase and a DNA-binding protein. A damage recognition complex composed of 2 uvrA and 2 uvrB subunits scans DNA for abnormalities. When the presence of a lesion has been verified by uvrB, the uvrA molecules dissociate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00211; ABC_TRANSPORTER_1; 2.
PROSITE; PS5083; ABC_TRANSPORTER_2; 1.
SGS response; Excision nuclease; DNA replir; DNA recombination;
DNA excision, ATP-binding; DNA-binding; Repeat; Zinc; Metal-binding;
                                    15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
UV-RAGC system protein A (UvrA protein) (Excinuclease ABC subunit A)
UVRA OR RV1638 OR MT1675 OR MTCY06H11.02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Whole genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                            Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglmeder K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Deviln K., Feltwell T., Gentles S., Hamlin N., Holroyd E., Osborne J., Osborne J., Moule S., Murphy L., Oliver S., Osborne J., Quall M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;

Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;

Nature 393:537-544(1998).
                                                                                                                                                      Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1773;
    972 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PR00005; ABC tran; 2.
ProDom; PD000006; ABC transporter; 1.
TIGRPAMs; TIGR00630; uvra; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HAMAP; MF 00205; -; 1.
InterPro; IPR003439; ABC transporter.
InterPro; IPR004602; UvrA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AB007031; AAK45944.1; ALT_INIT.
PIR; A70619; A70619.
      PRT;
                                                                                                                                                                                                                                                                                MEDLINE=98295987; PubMed=9634230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; 285982; CAB06633.1; -.
                                                                                                                                        Mycobacterium tuberculosis.
      STANDARD;
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Tuberculist; Rv1638;
                                                                                                                                                                                                                                        SECUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
UVRA MYCTU
P94972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bishai W.;
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5

Gaps

18;

4; Indels

1; Mismatches

||| ||| ||| ||| RTPRSNPATYTGVFDKIRILFAATTEAKVRGYQP-GRF 742

904

8 8

-----RGIRPVGRF 31

15; Conservative

Matches

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                                                                                                                                                                              ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (By similarity). Subunity between the search for SUBUNIT: Forms a heterotetramer with uvrB during the search for lesions (By similarity). SUBCELJULAR LOCATION: Cytoplasmic (By similarity). SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. UVRA SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=MAFF303099;
MEDLINFS-1082930; PubMed=11214968;
MEDLINFS-21082930; PubMed=11214968;
MEDLINFS-21082930; PubMed=11214968;
Matanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,
Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
Takeuchi C., Yamada M., Tabata S.;
"Completer genome structure of the nitrogen-fixing symbiotic bacterium
Mesorhizobium loti.";
DNA Res. 7:331-338(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Probom, PD000006; ABC transporter; 1.
TIGREAMS; TIGR00630; uvra; 1.
PROSITE; PS00211; ABC_TRANSPORTER 1; 2.
SPROSITE; PS50893; ABC_TRANSPORTER 2; 1.
SOS response; Excision nuclease; DNA repair; DNA recombination; DNA excision; ATP-binding; DNA-binding; Repeat; Zinc; Metal-binding;
                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Res. 7:331-338(2000).
FUNCTION: The UvrABC repair system catalyzes the recognition and processing of DNA lesions. UvrA is an ATPase and a DNA-binding protein. A damage recognition complex composed of 2 uvrA and 2 uvrB subunits scans DNA for abnormalities. When the presence of lesion has been verified by uvrB, the uvrA molecules dissociate
                                                                                                                                                                                                                                                                                                                                                                                                    28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
UvrABC system protein A (UvrA protein) (Excinuclease ABC subunit A)
UVRA OR MLR0750.
                                                                                                                                                                              18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Phyllobacteriaceae; Mesorhizobium.
                                                                                                                                     29.9%; Score 52; DB 1; Length 972; 39.5%; Pred. No. 11; ive 1; Mismatches 4; Indels
                  32 39 ATP (POTENTIAL).
257 285 C4-TYPE (ATYPICAL).
654 661 ATP (POTENTIAL).
753 779 C4-TYPE.
972 AA; 106131 MW; 8937A764E592D981 CRC64;
                                                                                                                                                                                                                                                        708 RTPRSNPATÝTGVPDKIRTLPAATTEAKVRGYQP-GRF 744
                                                                                                                                                                                                                 11 RTPDINPAWYTG-------RGIRPVGRP 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATP (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                        973 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HAMAP; MF_00205; -; 1.
InterPro; IPR003439; ABC_transporter.
InterPro; IPR004602; UvrA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rhizobium loti (Mesorhizobium loti).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zinc-finger; Complete proteome.
NP BIND 34 41 AT
  Complete proteome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AP002995; BAB48277.1; -.
                                                                                                                                                                                                                                                                                                                                                                                             28-FEB-2003 (Rel. 41, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00005; ABC tran; 2.
                                                                                                                                                          Local Similarity 39.5
les 15; Conservative
                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=381;
  Zinc-finger;
                                                                                                                                                                                                                                                                                                                                                        UVRA RHILO
Q98M36;
                                                     NP_BIND
ZN_FING
SEQUENCE
                                                                                                                                       Query Match
                  NP BIND
ZN_FING
                                                                                                                                                                                                                                                                                                                 RESULT 10
UVRA_RHILO
                                                                                                                                                                            Matches
STFFFS
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-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. UVRA SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Regulation of divergent transcription from the uvrA-ssb promoters in Sinorhizobium mellioti.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
VOYABC system protein A (UVAA protein) (Excinuclease ABC subunit A).
UVAA OR R01557 OR SMC01235.
Rhizobium meliloti (Sinorhizobium meliloti).
Bacteria, Proteobacteria, Alphaproteobacteria; Rhizobiales;
Rhizobiaceae, Sinorhizobium/Ensifer group; Sinorhizobium.
                                                                                                        Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       uvrB subunits scans DNA for abnormalities. When the presence of lesion has been verified by uvrB, the uvrA molecules dissociate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=21396507; PubMed=11481430;

Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,

Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,

Godrie T., Goffeau A., Boutry M., Cadieu B., Dreano S., Gloux S.,

Pohl T., Portetelle D., Rahn D., Kiss B., Lelaure V., Masuy D.,

Renard C., Thebault P., Vandenbol M., Weidner S., Galibert P.;

*Analysis of the chromosome sequence of the legume symbiont

Sinorhizobium meliloti strain 1021.";

Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
                                                                                                      18;
                                                                    Length 973;
                                                                                                      4; Indels
662 669 ATP (POTENTIAL).
761 787 C4-TYPE.
973 AA; 107358 MW; 767D7D2DC8220057 CRC64;
                                                                                                                                                                       716 RIPRSNPATYTGAFTPIRDWFAGLPEAKARGYOP-GRF 752
                                                                                                                                         11 RIPDINPAWYIG------RGIRPVGRF 31
                                                                  Score 52; DB 1;
Pred. No. 11;
1; Mismatches 4
                                                                                                                                                                                                                                                            973 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00005; ABC tran; 2.
ProDom; PD000006; ABC transporter; 1.
TIGRPAMs; TIGR00630; Uvra; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JAMAP, MF 00205, -; 1.
InterPro; IPR003439; ABC transporter.
InterPro; IPR004602; UvrĀ.
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                                                                  29.9%;
39.5%;
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                                                                                   Local Similarity 39.5 tes 15; Conservative
                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tapias A., Barbe J.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=382;
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P56899;
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InterPro; I
NP_BIND
ZN_FING
SEQUENCE
                                                                    Query Match
                                                                                                                                                                                                                            RESULT 11
UVRA RHIME
                                                                                                     Matchee
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gene.";
Gene 177:23-28(1996).
[3]
                                                                                                     MIM; 604617; -.
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ACT_SITE
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-FEB-2003 (Rel. 41, Last annotation update)
Sialidase 3 (EC 3.2.1.18) (Membrane sialidase) (Ganglioside sialidase)
(N-acetyl-alpha-neuraminidase 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUR=Brain;
MEDLINE=99335353; PubMed=10405317;
Wada T., Yoshikawa Y., Tokuyama S., Kuwabara M., Akita H., Miyagi T.;
"Cloning, expression, and chromosomal mapping of a human ganglioside
                                                                                                                                                                                                                                                                                          Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               glycoconjugates.
CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-,
alpha-(2->8)-glycosidic linkages of terminal sialic residues in
oligosaccharides, glycoproteins, glycolipids, colominic acid and
synthetic substrates.
PROSITE; PS00211; ABC_TRANSPORTER_1; 2.
PROSITE; PS50893; ABC_TRANSPORTER_2; 1.
SOS response; Excision nuclease; DNA repair; DNA recombination;
DNA excision; ATP-binding; DNA-binding; Repeat; Zinc; Metal-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PubMed=10861246; Marsoni M., Riboni M., Manzoni M., Venerando B. Monti E., Bassi M.T., Papini N., Tettamanti G., Borsani G.; Preti A., Ballabio A., Tettamanti G., Borsani G.; "Identification and expression of NEU3, a novel human sialidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -i- TISSUE SPECIFICITY: Highly expressed in skeletal muscle, testis, adrenal gland and thymus, followed by pancreas, liver, heart and thymus. Weakly expressed in kidney, placenta, brain and lung.
-i- MISCELLANBOUS: Optimum pH is 3.8
-i- SIMILARITY: BELONGS TO PAMILY 33 OF GLYCOSYL HYDROLASES.
-i- SIMILARITY: Contains 3 BNR repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            heart and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               associated to the plasma membrane.";
Biochem. J. 349:343-351(2000).
-1- FUNCTION: Plays a role in acculating the ganglioside content of the lipid bilayer at the level of membrane-bound sialyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ..... osp. parazona, Mordata, Craniata, Vertebrata, Buteleostomi,
Bukaryota, Metazona, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                        18;
                                                                                                                                                                                                                                              Score 52; DB 1; Length 973; Pred. No. 11; Mismatches 4; Indels
                                                                                                11 RTPDINPAWYTG----------RGIRPVGRP 31
                                                                                                                                                                                                                                                                                        4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Biochem. Biophys. Res. Commun. 261:21-27(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: Membrane-associated.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         428 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Rel. 41, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NER3 HUMAN STANDARD;
Q9UQ49; Q9NQE1;
28-PEB-2003 (Rel. 41, Created)
                                                                                    Complete proteome
                                                                                                                                                                                                                                                29.9%;
                                                                                                                                                                                                                                                                     39.5%;
                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Skeletal muscle;
                                                                                                                          669
787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human)
                                                                                                                        662
761
19
67
973 AA;
                                                                                                                                                                                                                                                                   Local Similarity
hes 15; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
                                                                                Zinc-finger; (NP_BIND 66 ZN_FING 76 CONFLICT 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-FEB-2003
Sialidase 3
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                                                                                                                                                                                   CONFLICT
                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 12
NER3_HUMAN
                                                                                                                                                                                                                                                                       Best Loc
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rielschmann R.D., Adams M.D., White O., Clayton R.A., Kirkness B.P., Korlavage A.R., Bult C.J., Tomb J.-P., Dougherty B.A., Merrick J.M., McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.P., Phillips C.A., Spriggs T., Hedblom B., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fine L.D., Pritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8
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MRDLINE-37080495;
MRD MROPARAM M.L., Hendrixson D.R., St Geme J.W. III;
Replation and characterization of the Haemophilus influenzae uvrA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P444I0; Q48151;
01-NOV-1995 (Rel. 32, Created)
1-NOV-1995 (Rel. 32, Last sequence update)
28-FKB-2003 (Rel. 41, Last annotation update)
UVRABC system protein A (UVRA protein) (Excinuclease ABC subunit UVRA OR H10249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria, Proteobacteria, Gammaproteobacteria, Pasteurellales,
Pasteurellaceae, Haemophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29.3%; Score 51; DB 1; Length 428; 33.3%; Pred. No. 6.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Potential.
35D1DD9359A78C98 CRC64;
                                                                                                                                GO; GO:0005887; C:integral to plasma membrane; TAS. GO:0006689; P:ganglioside catabolism; TAS. Interpro; IPR002860; GH_BNR. PR02012; BNR; 3. Hydrolase; Glycosidase; Membrane: Reneat
                                                                                                                                                                                                                                                                                                                                                                                           By similarity.
Potential.
Potential.
                                                                                                                                                                                                                                                     3 Glycosidase; Membrane; Repeat.
129 140 BNR 1.
203 214 BNR 2.
24 27 FRIP MOTIF.
25 25 By similarity.
45 45 Potential.
67 87 Potential.
87 87 Potential.
225 225 Potential.
225 225 Potential.
340 340 By similarity.
340 340 By cential.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    By similarity
Potential.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 RAHQHSMETRTPDINPAWYTGRGIRPV 28
send an email to license@isb-sib.ch)
                                              EMBL; AB008185; BAA82611.1; -.
EMBL; Y18563; CAB96131.1; ALT_INIT
Genew; HGNC:7760; NEU3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. STRAIN=Rd / KW20 / ATCC 51907;
STRAIN=Rd / KW20 / ATCC 51907;
MEDLINE=95350630;
WHOLINE=95350630;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   48252 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Haemophilus influenzae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       387
428 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
Matches 9; Conserv
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Pasteurella multocida.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
                                      NCBI_TaxID=747;
UVRA OR PM1951
                                                                                                                                                                                                                                                                                                                                                                                                                                                    NP_BIND
ZN_FING
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 15
LMBT HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mee by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3
                                                                                                                    (By similarity).
-!- SUBUNIT: Forms a heterotetramer with uvrB during the search for lesions (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. UVRA SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
       Pfam; PF00005; ABC_tran; 2.
Probon; PD00006; ABC_transporter; 1.
TIGREAMS; TIGR00630; uvra; 1.
PROSITE; PS00211; ABC_TRANSPORTER_1; 2.
PROSITE; PS50893; ABC_TRANSPORTER_2; 2.
SOS response; Excision nuclease; DNA repair; DNA recombination; DNA excision, ATP-binding; DNA-binding; Repeat; Zinc; Metal-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
UvrABC system protein A (UvrA protein) (Excinuclease ABC subunit A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29.3%; Score 51; DB 1; Length 943; 39.5%; Pred. No. 15; tive 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              104366 MW; 4DBA0DCFA602D465 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REF. 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KTPRSNPATYTGLFTPIRELFAGVPEARARGYNP-GRF 731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11 RTPDINPAMYTG------RGIRPVGRF 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            I -> M (IN REF. 2
E -> Q (IN REF. 2
A -> T (IN REF. 2
T -> B (IN REF. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                            ATP (POTENTIAL).
C4-TYPE.
V -> L (IN REF. 3
E -> D (IN REF. 3
R -> K (IN REF. 3
                                                                                                                                                                                                                                                                                                                                                                                                                         ATP (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               943 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FLKPILEK
                                                                                                                                                                                                                                                                                                               HAMAP; MF 00205; -; 1.
InterPro; IPR003439; ABC transporter.
InterPro; IPR004602; UvrĀ.
                                                                                                                                                                                                                                                                                                                                                                                                                                  C4-TYPE
                                                                                                                                                                                                                                                                                                                                                                                                               Complete proteome
                                                                                                                                                                                                                                                            EMBL; U32711; AAC21915.1; -. EMBL; U33877; AAC44592.1; -. EMBL; U04997; AAA60462.1; -. PIR; D64057; D64057.
  OF 1-71 FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 39.5
nes 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             943 AA;
                                                                                                                                                                                                                                                                                            PIR; D64057; L
TIGR; HI0249;
                                                                                                                                                                                                                                                                                                                                                                                                               Zinc-finger; (NP_BIND ZN_FING 29 NP_BIND 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             UVRA PASMU
P57979;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZN_FING
CONFLICT
CONFLICT
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CONFLICT
CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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ID UVRA P1
AC P57979
DT 16-OCT
DT 28-FEB
DE UVYABC
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    lesions (By similarity).
    SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
    SIMILARITY: BELONGS TO THE ABC TRANSPORTER PAMILY. UVRA SUBFAMILY.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HAMAP, MF_00205; -; 1.
InterPro; IPR003493 ABC transporter.
InterPro; IPR004602; UvrA.
Pfam; PR004005; ABC tran; 2.
Probom; PD000006; ABC transporter; 1.
PTGRPAMs; TIGR0630; UvrA; 1.
PROSITE; PS00211; ABC TRANSPORTER_1; 2.
PROSITE; PS50933; ABC TRANSPORTER_1; 2.
SGS response; Excision nuclease; DNA repair; DNA recombination;
DNA excision; ATP-binding; DNA-binding; Repeat; Zinc; Metal-binding;
Zinc-finger; Complete proteome.
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                                                                                                                                                                                                                                                                                                                                                         LMBT HUMAN STANDARD; PRT; 772 AA.
09Y466; Q9H186; Q9H1G5; Q9UG06; Q9UJB9; Q9Y4C9;
28-F8B-2003 (Rel. 41, Created)
15-SBP-2003 (Rel. 42, Last sequence update)
15-SBP-2003 (Rel. 41, Last sequence update)
15-SBP-2003 (Rel. 42, Last sequence update)
15-SBP-2003 (Rel. 41, Last sequence update)
15-SBP-2003 (Rel. 41, Last sequence update)
15-SBP-2003 (Rel. 42, Last sequence updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SUBUNIT: Forms a heterotetramer with uvrB during the search for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalla, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18;
Bacteria, Proteobacteria, Gammaproteobacteria, Pasteurellales;
Pasteurellaceae, Pasteurella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 51; DB 1; Length 943;
Pred. No. 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATP (POTENTIAL).
28 C4-TYPE.
47 ATP (POTENTIAL).
66 C4-TYPE.
104186 MW; A096DB1162D3C354 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          695 RIPRSNPATYTGLFTPIRELFAGVPESRARGYNP-GRF 731
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                              STRAIN=Pm70;
MEDLINE=21145866; PubMed=11248100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AB006231; AAK04035.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 29.3%;
Best Local Similarity 39.5%;
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human)
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MEDINE-98403880; PubMed=9734811;
MEDINE-98403880; PubMed=9734811;
MA Ishikawa K.-I., Nagase T., Suyama M., Miyajima N., Tanaka A.,
Kotani H., Nomura N., Ohara O.;
Mara O.;
The complete sequences of 100 new cDNA clones from brain which can code for large proteins in vitro.";
The complete sequences of 100 new cDNA clones from brain which can code for large proteins in vitro.";
DNA Res. 5:169-176(1998).
IL DNA Res. 5:169-176(1998).
C-I-FUNCTION: Polycomb group (PcG) protein. PcG proteins maintain the transcriptionally repressive state of genes, probably via a modification of chromatin, rendering it heritably changed in its expressibility. Probably plays a role in cell proliferation.
Coverexpression induces multimuclated cells, suggesting that it is required to accomplish normal mitosis.
C-I-SUBCELULAR LOCATION: Nuclear; excluded from the nucleolus. Does two proteins do not belong to the same complex.
C-I-ALTERNATIVE PRODUCTS:
C-I-ALTERNATIVE P
                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=216180749; PubMed=11780052;

MEDLINE=216180749; PubMed=11780052;

Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
Jones M., Stavindes G., Almedda J.P., Babbage A.K., Bagguley C.L.,
Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
Bailey J., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
Blington A.G., Frankland J.A., Fraser A., French L., Garner P.,
Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
Hunmond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson D.,
Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
Lehvaeslaiho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
Marsh V.L., Martin S.L., McConnachie L.J., McLay, Rawash Y.L.,
Mills S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
A Rice C.M., Ross M.T., Socht C.E., Showhkeen R., Sins S.,
Swuce C.D., Smith M.L., Sochtlund C., Steward C.A., Sulston J.E.,
Milliance B.J.C.T., Prartalingam S.R., Plumb R.W., Thorpe A.,
Swann R.M., Sycamore N., Taylor R., Tee L., Thomass D.W., Thorpe A.,
Milning L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Williams S.A.,
Williang L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R.,
Milning L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R.,
M. Horer H.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isold=09Y468-4; Sequence=VSP_003903; TISSUE SPECIFICITY: Widely expressed. Expression is reduced in
                                                                                                                                          "A human homolog of Drosophila lethal(3)malignant brain tumor (1(3)mbt) protein associates with condensed mitotic chromosomes."; Oncogene 18:3799-3809(1999).
                             TISSUE=Brain;
MEDLINE=99373015; PubMed=10445843;
Koga H., Matsul S.-I., Hirota T., Takebayashi S.-I., Okumura K.,
                                                                                                                                                                                                                                                                                                                                               Koehrer K., Beyer A., Mewes H.-W., Gassenhuber J., Wiemann S.;
Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IsoId=Q9Y468-3; Sequence=VSP_003901, VSP_003902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Event=Alternative splicing; Named isoforms=4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 215-772 FROM N.A. (ISOFORM 4).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Name=1; Synonyms=mbt-I;
IsoId=Q9Y468-1; Sequence=Displayed;
SEQUENCE FROM N.A. (ISOPORMS 1 AND 2)
                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORM 3).
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                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                 TISSUE=Uterus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rissum=Brain;
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                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ARIVEVITYSERTLYWITYAQLGDLYCSDHLQBGKGILETGY HSLLCSLPTHLLAKLSFASDSQY -> VRCKCRVGDRAGVT VLKTAGSRCPPQRHPC (in isoform 2 and isoform 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /FTIG=VSP 003902.
ARIVRVTHVŠGKTLVWTVAQLGDLVCSDHLQECKGILETGV
HSLLCSLPTHLLAKLSFASDSQY -> MIDGRAFLLLTQAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSLLCSLPTHLLAKLSFASDSQY -> MIDGRAFLLLTQAD
IVKIMSVKLGPALKIYNAILMFKNADDTLK (in
                                                                              telophase.
SIMILARITY: Contains 3 mbt domains.
CAUTION: Ref.3 (CAC18508) sequences differ from that shown due to erroneous gene model prediction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
colorectal cancer cell line SW480 and promyelocytic leukemia cell
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                            DEVELOPMENTAL STAGE: In interphase cells, it is scattered throughout the nucleoplasm. In mitotic cells, it strongly associates with condensed chromosomes from the prophase to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transcription regulation; Chromatin regulator; Zinc-finger; DOMA-binding; Nuclear protein; Repeat; Alternative splicing. DOMA.N 242 315 MBT 1. Alternative splicing. DOMAIN 349 422 MBT 2. MBT 2. ZOMAIN 453 526 MBT 3. ZOMAIN 453 526 ZOMAIN 453 526 WBT 3. ZOMAIN 453 548 CZHC-TYPR.
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/FIId=VSP 003903.
P -> L (IN REF. 1).
LR -> MC (IN REF. 1).
L -> M (IN REF. 1).
S -> P (IN REF. 1).
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                                                                                                                                                                                                                                                                                      EMBL, U89358; AAC69438.1; -.
EMBL, AL110279; CAB5714.1; -.
EMBL, 289752; CAC16799.1; -.
EMBL, 298752; CAC16800.1; -.
EMBL, 298752; CAC18508.1; -.
EMBL, AL031681; CAC17518.1; ALT_SEQ.
EMBL, AL031681; CAC17518.1; ALT_SEQ.
EMBL, AB014581; BAA31656.1; -.
EMBL, T14794; T14794.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Genew, HGNC:15905, L3MBTL.
GEN, Q0X468, -.
InterPro; IPR004092; Mbt.
InterPro; IPR002515; Znf_C2HC.
Pfam, PF02820, mbt; 3.
Pfam, PF01530; zf-C2HC.
Pfam, PR01530; zf-C2HC.
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332
595
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332
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772 AA;
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Title: Perfect score:

Run on:

Sequence:

Scoring table:

Searched:

Minimum DB Maximum DB

Database

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Q8dcj3 vibrio vuln
Q8dgi0 corynebacte
Q8kz57 uncultured
Q8kz57 uncultured
Q8yvi8 peeudomonas
Q8tv8 methanosarc
Q8ywc7 anabaena sp
Q8tv6 arabidopsis
Q8yhc4 brucella me
Q8dj0 brucella me
Q8dj0 brucella me
Q8dj0 brucella me
Q8dm52 synechococc
Q9kxy1 vibrio chol
Q96d4 homo sapien
Q8ixt2 homo sapien
                                                                                                                                                                                                                                                                                                                   Q9rji0 streptomyce
Q818a7 arabidopsis
O33480 propionibac
                                                                                                                                                                                                                                                                                                                                                                                                 Q81uv7 homo sapien
Q9vrv3 drosophila
Q8fb02 escherichia
                                                                                                                                                                                                                                                                                                                                                                   Q8nnc6 corynebacte
Q91fa0 arabidopsis
 Q8xni5 clostridium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. Curlewis J.D., Anderson S.T., Curlewis J.D., Kusters D.H.L., Barclay J.L., Anderson S.T., "Prolactin-releasing peptide (PrRP) in the ewe: cDNA cloning, mRNA distribution and effects on prolactin secretion in vitro and in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Preproprolactin-releasing peptide.

Ovis aries (Sheep).

Bukaryota, Metazooa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;

Bovidae; Caprinae; Ovis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         / Match 93.7%; Score 163; DB 6; Length 98; Local Similarity 93.5%; Pred. No. 5.7e-16; nes 29; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 vivo.";
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF450453; AAL47178.1; -.
SEQUENCE 98 AA; 10513 MW; 2A53331ED62CAABS CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q8WN12;
Q8WN12;
Q8WN12;
Q8WN12;
Q8WN12;
Q9WN12;
Q9WN12;
Q1-MAR-2002 (TrEMBLrel. 20, Created)
Q1-MAR-2002 (TrEMBLrel. 20, Last sequence update)
Q1-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
Last sequence update)
Last annotation update)
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QBXN15
QBNC73
QBNC73
QBPTQ6
QBFTQ6
QBFTS7
QBFWC7
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QBFWC7
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QBFWC2
QBFWC4
QB
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Q96SD4
Q8N6Q2
Q8IXT2
Q8CGW9
Q8CSY9
Q08SS78
Q09KJ10
Q9RJ10
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QBNNC6
 (TrEMBLrel. 12, TrEMBLrel. 12, TrEMBLrel. 19,
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 Q9W624;
Q9W624;
01-NOV-1999 (
01-NOV-1999 (
01-DEC-2001 (
Query Match
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QBWN12
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                                                                                                 December 3, 2003, 19:03:25 ; Search time 26.5 Seconds (without alignments) 301.873 Million cell updates/sec
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
              GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                             1 SRAHQHSMETRTPDINPAWYTGRGIRPVGRF 31
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                                                                                                                                                                                                                                                                       830525 seqs, 258052604 residues
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Maximum Match 100%
Listing first 45 summaries
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Q9W624
Q9U845
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Q9UPA4
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Q9STB
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Q8HP9
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Q8BHP9
Q8TBF
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sp_virus:*
sp_vertebrate:*
sp_unclassified:*
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Gapop 10.0 , Gapext 0.5
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1: sp_archea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*
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174
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692
1253
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Score

Result

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mechanisms and effects (Proceedings of the 11th international congress on photosynthesis), pp.4:2889-2892, Kluwer Academic Publishers,
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MEDLINE=21822632; PubMed=11832943;
MEDLINE=21822632; PubMed=11832943;
Beja O., Suzuki M.T., Heidelberg J.F., Nelson W.C., Preston C.M.,
Hamada T., Eisen Fraser C.M., DeLong B.F.;
"Unsuspected diversity among marine aerobic anoxygenic phototrophs.";
Nature 415:630-633 (2002).
EMBL; AE008919; AAL76369.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Dark aerobic growth conditions induce the synthesis of a high midpoint potential cytochrome c8 in the photosynthetic bacterium midpoint potential cytochrome c8 in the photosynthetic bacterium Rubrivivax gelatinosus.";

Biochemistry 38:15238-1524(1999).

EMBL; AB034704; BAA94057.1; -..

EMBL; AB034704; DR03572; CobN/Mg_chltase.

Pfam: PP02514; cobN-Mg_chltase.

Transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=94132007; PubMed=8300574; Magashima K.; Matumima K.V.; Matumima K.V.; Matumima K.O.; Matumima Matumi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Menin L., Yoshida M., Jaquinod M., Nagashima K.V., Matsuura K.,
Parot P., Vermeglio A.;
                                                                                                                                                                    "Phylogenetic analysis of photosynthetic genes of Rhodocyclus gelatinosus: Possibility of horizontal gene transfer in purple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=IL144;
Igarashi N., Shimada K., Matsuura K., Nagashima K.V.;
"Photosynthetic gene cluster in purple bacterium, Rubrivivax
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 61; DB 2; Length 1236;
Pred. No. 5.6;
6; Mismatches 8; Indels
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
CobN/magnesium chelatase family protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  uncultured proteobacterium.
Bacteria; Proteobacteria; environmental samples.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 AHQHSMETRIPDINPAWYTG-----RGIRPV 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT; 1253 AA.
                                                                                  STRAIN=1L144;
Nagaghlma K.V., Shimada K., Matsuura K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             J. Biol. Chem. 269:2477-2484(1994)
[3]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=1L144;
MEDLINE=20031519; PubMed=10563807;
                                                                                                                                                                                                                                                                                               Photosyn. Res. 36:185-191(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 37.5%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Photos.";
gelatinosus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=153809;
[1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE PROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dordrecht (1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EBAC000-65D09.24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gelatinosus.";
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SOW KENT THE RESERVE THE RESER
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                                                                        Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostel; Ostariophysi; Cypriniformes;
Cyprinidae; Carassius.
NCBI_TaxIb=7957;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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"Role of the H protein in assembly of the photochemical reaction
enter and intracytoplasmic membrane in Rhodospirillum rubrum.";
J. Bacteriol. 182:1200-1207 (2000).

EMBL; AF202319; AAF37352.1;

EnterPro; IPR003672; Cobn/Mg_chltase.
Pfam; PF02514; cobn/Mg_chltase.

NON TER
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Rhodospirillaceae, Rhodospirillum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Comamonadaceae; Rubrivivax.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    39.1%; Score 68; DB 2; Length 692;
43.8%; Pred. No. 0.29;
tive 4; Mismatches 8; IndelB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3; Indels
                                                                                                                                                                                                                                                                                                                                                                                 Satake H., Minakata H., Fujimoto M.;
"Carassius RFamide (C-RF amide) ";
Submitred (NOV-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AB020024; BAAA5662.1; -.
SEQUENCE 117 AA; 12879 MW; D5DC4CB22038C2B0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           692 AA; 75453 MW; 96430AE93BF35680 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         / Match 61.5%; Score 107; DB 13
Local Similarity 57.7%; Pred. No. 9e-08;
Ne 15; Conservative 8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 AHQHSMETRTPDINPAWYTG-----RGIRPV 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   692 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mg protoporphyrin methyl transferase BCHH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=20138142; PubMed=10671438;
                                             Carassius auratus (Goldfish).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Guery Match
Best Local Similarity 43.8%;
Matches 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. TISSUE=Brain;
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C-RF amide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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Query Match
32.2%; Score 56; DB :
Best Local Similarity 36.7%; Pred. No. 7.5;
Matches 11; Conservative 8; Mismatches
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Best Local Similarity 50.0%
Similarity 50.0%
Similarity 50.0%
Similarity
                                                                                                                                                  PRELIMINARY;
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                                                                                                                                                                                                                                        Homo sapiens (Human)
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                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
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Q8BHP9;
01-MAR-2003 (
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MEDLINE=99061957; PubMed=9843979;
Miong J., Inoue K., Bauter C.B.;
Tracking molecular evolution of photosynthesis by characterization of a major photosynthesis gene cluster from Heliobacillus mobilis.";
Proc. Natl. Acad. Sci. U.S.A. 95:14851-14856(1998).
EMBL; AF080002; ARC84033.1; -.
InterPro; IPR03572; CobN/Mg_chltase.
Fram; PF02514; cobN-Mg_chli.1.
SEQUENCE 1292 AA; 144854 MW; 323AA0517807448D CRC64;
                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                       Bacteria; Firmicutes; Clostridia; Clostridiales; Heliobacteriaceae;
Heliobacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Phlebobranchia; Cionidae; Ciona.
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                                                  Length 1253;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Imai K.S., Satoh N., Satou Y.;
"Ciona savignyi genes";
"Ciona davignyi genes";
"Ciona savignyi genes";
"Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AB057747; BAB68356.1;
"InterPro; IPR001087; Znf C2H2.
"Fran; PP00096; Zf-C2H2; 4.
PR0STTE; PS00028; ZINC FINER C2H2.1; 3.
PROSITE; PS0157; ZINC FINER C2H2.2; 4.
Metal-binding; Zinc; Zinc-finger.
SEQUENCE 355 AA; 40876 MW; ES8FSDEDDB12E8AC CRC64;
Interpro; IPR003672; CobN/Mg_chltase.
Pfam; PF02514; cobN-Mg_chel; 1.
SEQUENCE 1253 AA; 137586 MW; C98ABC010E261511 CRC64;
                                                                           Indels
                                                                                                                                                                                                              01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAY-2002 (TrEMBLrel. 20, Last annotation update)
Mg chelatase subunit H BchH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DAR-2003 (TrEMBLrel. 23, Last annotation update)
Zic related protein la.
                                                3; DB 2;
                                                                                                               3 AHOHSMETRIPDINPAWYTG-----RGIRPV 28
                                                                                                                                                                                       PRT; 1292 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      355 AA
                                                 Query Match
33.3%; Score 58; DB
Best Local Similarity 37.5%; Pred. No. 15;
Matches 12; Conservative 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1176 ETRIKTLNPKWYEGMLKHGYEGVREI 1201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9 ETRTPDINPAWYTG-----RGIRPV 28
                                                                                                                                                                                       PRELIMINARY;
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                                                                                                                                                                                                                                                                            Heliobacillus mobilis.
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                                                                                                                                                                                                                                                                                                                NCBI_TaxID=28064;
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Q95YJ8
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STRAIN=C57BL/61; TISSUE=Body;

STRAIN=22554681; PubMed=12466851;

The FANTOM Consortium.

The FANTOM Consortium.

The RIKEN Genome Exploration Research Group Phase I & II Team;

"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";

Nature 420:563-573 (2002).

ENBL; AK017751; BAC25529.1; -.

Hypothetical protein.

SEQUENCE 139 AA; 14740 MW; A08DD1B09441B259 CRC64;
                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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DB 5, Length 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 30.5%; Score 53; DB 4; Length 54; Best Local Similarity 50.0%; Pred. No. 2.6; Matches 8; Conservative 1; Mismatches 7; Indele
                                                    7; Indels
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SEQÜENCE 54 AA; 6110 MW; E2F3C39F7B961A9F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Weakly similar to hypothetical protein KIRA0574.
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                    01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DJ479J7.3 (Sushi-repeat protein (SRPUL)) (Fragment)
                                                                                                                                                                                                                                                                                            54 AA.
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                                                                                                                                  27 QAHQHSIDSKPMQLNSVPSAAYYAGYGMIP 56
                                                                                                       2 RAHQHSMETRTPDIN----PAWYTGRGIRP 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               47 HQHS-STGDPD---TWKTGQGTKP 66
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                                                                                                                                                                                                                                                                                                                                              01-MAY-2000 (TrEMBLrel. 13, Created)
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Gaps
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Strausberg R.,
Strausberg R.,
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
C -1- SIMILARITY: BELONGS TO THE COLD-SHOCK DOMAIN (CSD) FAMILY.
REMEL, BC024836; AAH34936.1; -.
R InterPro; IPR002059; Cold_shock.
R InterPro; IPR002059; Cold_shock.
R Problom; PP00313; CSD; 7.
R Problom; PP00313; CSP; 4.
SMART; SM00357; CSP; 4.
R PROSITE; PS00436; PEROXIDASE_2; 1.
R PROSITE; PS00436; PEROXIDASE_2; 1.
NON_TER
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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   30.5%; Score 53; DB 4; Length 465; S0.0%; Pred. No. 27; tive 1; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Strausberg R.;
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC020733; AAH20733.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IRR01128; Cytochrome_P450.
InterPro; IRR001128; Cytochrome_P450.
InterPro; IRR001416; Hyalin.
InterPro; IRR000436; Sushi_SCR_CCP.
Pfam; PF00044; HYR; 1.
Pfam; PF000084; Sushi; 3.
SMART; SM00022; CCP; 3.
PROSITS; PS000086; CYTOCHROME_P450; 1.
SEQUENCE 465 AA; 52957 MW; 3D7229487DA1B8BD_CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical 76.9 kba protein (Fragment).
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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                                                                                                                                                                  18 TPAVTPTWYAGSGYYP 33
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Query Match
Best Local Similarity 50.0%
Matches 8; Conservative
                                                                                                                      12 TPDINPAWYTGRGIRP
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Best Local Similarity
Matches 8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                          QBWW85;
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"Cloning and characterization of the sushi-repeat containing protein (SRP) as a novel interaction partner of Rh type C glycoprotein (RhCG).";
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF060567; AAC15765.1;
EMBL; AF393649; AAM73693.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Kurosawa H., Innkai T., Inaba T., Goi K., Chang K.-S., Sinjyo T.,
Rakestraw K.M., Naeve C.W., Look T.A.;
Submitted (Apr-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18;
                                                                                                                                                                                                                                          Prevotella albensis.
Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
Prevotellaceae; Prevotella.
NCBI_TAXID=77768;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 30.5%; Score 53; DB 2; Length 223; Best Local Similarity 39.5%; Pred. No. 12; Matches 15; Conservative 1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=M384;
Walker N.D., McEwan N.R., Wallace R.J.;
Walker N.D., McEwan N.R., Wallace R.J.;
Submitted la albenis putative uvrA gene.";
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
-i.—SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY.
EMBL; AP070990; AAC241312;
InterProj IPRO03439; ABC transporter.
ProDom; PD000006; ABC transporter; 1.
PROSITE; PS00211; ABC TRANSPORTER; 1.
ATP-binding; Transport.
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01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Sushi-repeat protein (Sushi-repeat containing protein)
SRPUL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       223
24579 MW; 2563BA0B0C2996C9 CRC64;
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                                                                                                                                Created)
Last sequence update)
Last annotation update)
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                                                                       223 AA
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InterPro; IPR003410; Hyalin.
InterPro; IPR000436; Sushi_SCR_CCP.
                                                                                                                                                                                                                    Excinuclease ABC subunit A (Fragment)
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Pfan; PF002494; HYR; 1.
PROSITE; PS00006; CYTOCHROME P450; 1.
SEQUENCE 465 AA; 52971 WW; 4D7521
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                                                                       PRT;
                                                                                                                             01-NOV-1998 (TrEMBLrel. 08, 01-NOV-1999 (TrEMBLrel. 12,
                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 9-191 FROM N.A.
                                                                                                                                                                                           01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                       PRELIMINARY;
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SEQUENCE
                                                                                                    085605
                                                                    085605
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         RESULT 10
085605
DD 08560
DT 01-NO
DT 01-NO
DD 01-NO
DD 01-NO
DD 01-NO
DD 08560
DD 01-NA
DD 0
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Search completed: December 3, 2003, 19:14:01
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L. Sumitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.

C. 1- SIMILARITY: BELONGS TO THE COLD-SHOCK DOMAIN (CSD) FAMILY.

R. EMBL; BC02968; AAH29681; -.

R. MGD; MGI:92356; D3Jfr1.

R. MGD; MGI:92356; D3Jfr1.

R. InterPro; IPR002059; Cold shock.

R. InterPro; IPR002059; Cold shock.

R. Ffam; PF00313; CSD; 8.

PFam; PF0004; P0006621; Cold shock; 1.

DR. PROSTIE; PS00435; COLD SHOCK; 4.

DR. PROSTIE; PS00435; COLD SHOCK; 4.

DR. PROSTIE; PS00436; PEROXIDASE 2; 2.

KW. HYPOTCHELICAL PROCEIN.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus

NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
NCBI_TaxID=10090;
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                                                  Query Match 30.5%; Score 53; DB 11; Length 689; Best Local Similarity 43.5%; Pred. No. 42; Matches 10; Conservative 5; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Strausberg R.;
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
689 AA; 76861 MW; 470743A80947A3A9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
10-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein MGC19174.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DRA-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical 88.8 kDa protein.
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                                                                                                                                                                                                                                                                                                                                                                             767 AA
                                                                                                                                                                                                        ||: ||: ||: ||: ||-: ||-: 474 HSVNGITEEANPTIYSGKVIRPL 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 HSMETRTPDINPAWYTGRGIRPV 28
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SEQUENCE FROM N.A.
TISSUE=Colon;
Strausberg R.;
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SEQUENCE
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Matches
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080ZN2
AC 080ZN2
DT 01-0C
DT 01-0C
DT 01-0C
DT 01-0C
DE HYPOT
DE HYPOT
DE HYPOT
DE NAMM
OC BURAR
OC C -1-S
DR REMBL;
DR REMBL;
DR REMBL;
DR REMBL;
DR REMBL;
DR REMBL;
DR PRODI
DR PFAM;
DR PRODI
DR PROSI
DR PROSI
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291W50
10 291W5
AC 091W5
DT 01-DE
DT 0
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Gaps
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Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.

-1. SIMILARITY: BELONGS TO THE COLD-SHOCK DOWAIN (CSD) FAMILY.

EMBL, BC016699; AAH1699.1; -.

MGD, MGI:92356; D34fe1.

InterPro; IPR002016; Peroxidase.

Propom; PP00113; CSD, 8.

Probom; PD000621; Cold_shock; 1.

PROSITE; PS000352; Cold_SHOCK; 4.

PROSITE; PS00436; PEROXIDASE_2; 2.
                                                                                                                                                                                                                                                                                                                                     Length 798;
                                                                                                                                                                                                                                                                                                                                                                                8; Indels
                                                                                                                                                                                                                                                                  11 protein.
798 AA; 88790 MW; 731065F734C60009 CRC64;
                                                                                                                                                                                                                                                                                                                                 Query Match
30.5%; Score 53; DB 11;
Best Local Similarity 43.5%; Pred. No. 50;
Matches 10; Conservative 5; Mismatches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 HSMBTRTPDINPAWYTGRGIRPV 28
                                                                                                                                                                                                                                                             Hypothetical
SEQUENCE 79
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Human oxytocin sec Human CRH releasin Peptide production Human type G prote

Peptide production

Human CRH releasin
Peptide production
Human type ligand
Human type ligand
Human cRH releasin
19P2 ligand peptid
Prolactin releasin
Bovine grotein-c
Bovine grotein-c
Bovine pituitary-d
Bovine pituitary-d
Bovine pituitary-d
Bovine pituitary-d
Bovine pituitary-d
Bovine pituitary-d
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19P2 ligand peptid
Bovine CRH releasi
Bovine CRH releasi

Bovine CRH releasi Peptide production Bovine G protein-c Bovine pituitary-d

19P2 ligand peptid Bovine CRH releasi

Bovine oxytocin se

Bovine G protein-c Bovine pituitary-d Bovine oxytocin se

OM protein

Run on:

Sequence:

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G protein-coupled receptor; ligand binding; pharmaceutical;
modulator; pituitary; central nervous system; pancreas; prophylactic;
therapeutic agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human type G protein-coupled receptor ligand fragment 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALIGNMENTS
                                                                                                                             AAB10361
AAG62530
AAY49299
                                                                                                                                                                                                                                                            AAG62516
AAE26399
ABU60825
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AAW95189
AAB10348
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ABU60832
AAW31373
                                                                              AAG62533
ABU60845
AAW31390
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AAY49290
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AAG62518
                                                        AAB10364
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                                             ABU60844
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96JP-0246573.
95JP-0343371.
96JP-0059419.
96JP-0211805.
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(TAKE ) TAKEDA CHEM IND LTD
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', Kitada C;
Hofno'sapiens.
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Kawamata Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-SEP-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10-JUL-1997
AAW31391;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW31393
RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human type ligand
Human 19P2 ligand.
Human oxytocin sec
19P2 ligand peptid
Human CRH releasin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Prolactin releasin
Human PrRP-31 pept
Peptide production
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                                                                           December 3, 2003, 18:57:14 ; Search time 33.75 Seconds (without alignments) 145.793 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                      A Geneseq 19Jun03:*

| SIDSIJgcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
| SIDSIJgcgdata/geneseq/geneseqp-embl/AA41981.DAT:*
| SIDSIJgcgdata/geneseqfy-embl/AA41981.DAT:*
| SIDSIJgcgdata/geneseqfy-embl/AA41991.DAT:*
| SIDSIJgcgdata/geneseqfy-embl/AA41993.DAT:*
| SIDSIJgcgdata/geneseqfy-embl/A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Description
           version 5.1.6
- 2003 Compugen Ltd.
                                                                                                                                                  1 SRIHRHSMEIRIPDINPAWYASRGIRPVGRF 31
                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                            1107863 seqs, 158726573 residues
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Maximum Match 100%
Listing first 45 summaries
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AAW87615
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AAG62531
AAB90991
AAB26401
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Gapop 10.0 , Gapext 0.5
         GenCore (c) 1993
                                                                                                                           US-09-868-885B-32
171
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seq length: 200000000
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Match
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Perfect score:
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Minimum DB Maximum DB

Database

20 4 5 9 7 8 9

Result

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The present sequence represents a human type ligand fragment. It
is used in the course of the invention. The specification describes
an agent for modulating prolactin secretion which comprises a
cligand polypeptide or a salt, for a G protein-coupled receptor (GPCR)
protein. The agents for promoting prolactin secretion can be used for
treating or preventing hypocovarianism, genecyst cacogenesis, menopausal
syndrome, enthyzoid or hypometabolism. They can by used for promoting
lactation in a domestic mammal and as an aphrodisiac. The agents for
inhibiting prolactin secretion can be used for treating or preventing
prolactinoma, infertility, impotence, amenorhea, galactorrhea,
acromegaly, Chiari-Frommel syndrome, Argonz-del Castilo syndrome,
corbes-Albright syndrome, lymphoma, Sheehan syndrome or dyszoospermia.
The inhibitory agents can also be used for treating or preventing
chodulating placental function can be used for treating or preventing
choricoarcinoma, hydatid mole, irruption mole, abortion, unthrifty fetus,
abnormal saccharometabolism, abnormal lipidmetabolism or oxytocia.
                                                          Use of G protein-coupled receptor ligands - for modulating prolactin secretion or placental function, e.g. for treating menopausal syndrome, tumours, autoimmune disease or abnormal pregnancy
                                                                                                                                                       Claim 3, Page 159; 241pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                  WPI; 1999-105614/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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                                                                                                                                                                     This sequence represents a peptide fragment from a novel human type ligand polypeptide corresponding to amino acid residues 23 to 53 of the sequence represented in AMM31390 and is used in an assay to monitor sequence represented in AMM31390 and is used in an assay to monitor ligand binding to the G protein-coupled receptor protein. Pharmaceutical compositions containing this ligand may be used as a pituitary function modulator. This ligand could have specific applications a central nervous system modulator or a pancreatic function modulator. This ligand could have specific applications of prophylactic or therapeutic agent for dementia, depression, hyperkinetic syndrome, solitophana, prowth hormone secretory disease, hyper- and polyphagia, hypertlipidaemia, hypercholesteroldemia, phypercaidaemia, hyperpolactinaemia, diabetes, cancer, pancreatitis, renal disease, hyperprolactinaemia, diabetes, cancer, pancreatitis, renal disease, hyperpolactinaemia, diabetes, cancer, pancreatitis, renal disease, hyperpolactinaemia, enerosis, asthoma, rheumatoid arthritis, spinal injury, transient brain ischaemia, epilepsy, amylotrophic lateral sclerosis, cute myocardial infarction, infertility, spinocerebellar degeneration, bone fracture, trauma, atopic dermatitis, osteoporosis and/or coligogalactia. Assays can also be developed to screen compounds which are capable of altering the binding activity of the ligand affecting activity of the ligand affecting
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rat type ligand; modulation; prolactin secretion; G protein-coupled receptor; GPCR; hypoovarianism; gonecyst cacogenesis; menopausal syndrome; euthyroid; hypometabolism; lactation; pitultary adenomatosis; brain tumour; emmeniopathy; autoimmune disease; prolactinoma; infertility; impocence; amenorrhaa; galactorrhaa; acromegaly; Chiari-Frommel syndrome; Argonz-del Castilo syndrome; Forbes-Albright syndrome; lymphoma; Sheehan syndrome; dyazoospermia; contraceptive; placental function; choriocarcinoma; hydatid mole; irruption mole; abortion; unthrifty fetus; abnormal saccharometabolism; abnormal lipidmetabolism; oxytocia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                   Ligand peptide for G protein-coupled receptor - acts by modulating function in the central nervous system, pancreas and pituitary gland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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100.0%; Pred. No. 5.8e-19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 SRTHRHSMEIRTPDINPAWYASRGIRPVGRF 31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human type ligand polypeptide fragment.
                                                                                                                                     Claim 2; Page 184; 258pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW97235 standard; peptide; 31 AA
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  WPI; 1997-363672/33.
N-PSDB; AAV02428.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31 AA;
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Gape

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100.0%; Score 171; DB 20; Length 31; 100.0%; Pred. No. 5.8e-19; ive 0; Mismatches 0; Indels (

1 SRITHRHSMEIRIPDINPAWYASRGIRPVGRF 31

31; Conservative

31 AA;

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Producing a 19P2 pituitary G protein receptor ligand - by cleavage of a fusion protein, useful for preventing and treating dementia, breast cancer, renal failure and autoimmune disease
                                                                                                                                                        19P2 ligand, G protein coupled receptor; pituitary; prolactin releasing peptide; human; dementia; breast cancer;
                                                                                                                                                                                                                                                                                                                                          Tanaka Y;
1 SRTHRHSMEIRTPDINPAWYASRGIRPVGRF
                                                                                                                                                                                                                                                                                                                                          Suenaga M,
                                                              AAW87615 standard; Peptide; 31 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 5; Page 35; 56pp; English.
                                                                                                                                                                                                                                                                                                                   (TAKE ) TAKEDA CHEM IND LID.
                                                                                                                                                                                                                                                                         98EP-0111725
                                                                                                                                                                                                                                                                                             97JP-0172118
                                                                                                              29-MAR-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                          Moriya T, Nishimura O,
                                                                                                                                                                                                                                                                                                                                                               WPI; 1999-047884/05.
                                                                                                                                  Human 19P2 ligand
                                                                                                                                                                                                                                                                         25-JUN-1998;
                                                                                                                                                                                                                                                                                             27-JUN-1997;
                                                                                                                                                                                                      Homo saplens
                                                                                                                                                                                                                            BP887417-A2
                                                                                                                                                                                                                                                  30-DEC-1998
                                                                                                                                                                                 cherapy.
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Human, oxytocin secretion promoter, G protein-coupled receptor protein, treatment, disease, pain, atonic bleeding, uterine recovery failure, cow, caesarean section, artificial fertilization, galactostasis, goat, pig,
                   This is the amino acid sequence of the human pituitary G
protein-coupled receptor ligand 19P2L. A method suitable for
commercial high-level production of 19P2L comprises expression
the ligand in host cells as a recombinant fusion protein e.g. with
human basic fibroblast growth factor (see AAV83796-97) that has
been modified to include an N-terminal cysteine residue. The
ligand is released from the fusion by cyanylation followed by
ammonolysis. 19P2L has prolactin secretion-stimulating and (at
high doses) prolactin secretion-inhibiting properties. It can be
used in the treatment and prevention of various diseases including:
senile dementia, cerebrovascular dementia, and dementia associated
with: genealogical disorders (e.g. Alzheimer's disease, Park's
disease, Pick's disease, Huntington's disease), infectious diseases
(e.g. Creutzfeldt-Jakob's), endocrine or metabolic disease or
croicosis (e.g. bypothyroidism, vitamin Bl2 deficiency, alcoholism,
intoxication by drugs, metal and organic compounds), tumourigenic
diseases (e.g. brain tumour), traumatic diseases (e.g. chronic
cubarachnoidal heamorrhage, and other types of dementia, depression,
hyperactive child syndrome (microencephalopathy) and disturbance of
consciousness. It is also useful for prevention and treatment of
disease associated with prolactin hypo and hypersecretion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               osteoporosis, menopausal syndrome and renal failure (hyposecretion disorders). The 19P2 polypeptide/amide is also useful as a test reagent for study of the prolactin secretory function or as a lactogogue in mammalian farm animals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      respectively, including: hyperprolactinaemia, pituitary adenoma, breast cancer, infertility, impotence and autoimmune disease (hypersecretion disorders), and seminal vesicle hypoplasia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human oxytocin secretion promoting peptide SEQ ID NO: 32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 171; DB 20; 100.0%; Pred. No. 5.8e-19;
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This invention describes a novel oxytocin secretion-regulating agent which contains a ligand peptide or its salt for the G protein-coupled receptor protein. It is useful in the form of drugs for amaliorating, preventing and treating diseases relating to oxytocin secretion e.g. weak pains and atonic bleeding, before and after expulsion of placenta, uterine recovery failure, caesarean section, stoppage of artificial fertilization or galactostasis and is also applicable in veterinary medicine for promoting milk production in cow, goat and pig. This sequence represents a human peptide which acts as an oxytocin secretion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention provides a monoclonal antibody which has a specific reaction with the part peptide of the C-terminal of 19P2 ligand or its derivative. The antibodies can be used in diagnosis or to treat or prevent diseases associated with abnormality in the pituitary function regulatory mechanism (e.g. provident of prolactin secretion), central nervous regulatory mechanism, and pancreatic function regulatory mechanism. The antibody-based immunoassay can also be applied in
protein-coupled receptor protein, for promoting secretion of oxytocin, as drugs for diseases relating to oxytocin secretion and in veterinary
                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Monoclonal antibody, 19P2 ligand; diagnosis; prolactin secretion; pituitary; regulatory mechanism; central nervous system; pancreatic.
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                                                                    Disclosure; Page 62; 72pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY49291 standard; peptide; 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19P2 ligand peptide fragment.
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Best Local Similarity
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Modified-Bite
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Gaps

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Indels

Length 31;

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Physiologically-active polypeptide recognized as ligand by

Hinuma S;

Matsumoto H, Kitada C, WPI; 2000-452298/39.

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Modifying and attaching therapeutic peptides to albumin prevents peptidase degradation, useful for increasing length of in vivo activity
                                                                                                         Protection, endogenous therapeutic peptide; peptidase; conjugation, blood component; modification; succinimidyl; maleimido group; amino; hydroxyl; thiol; hormone; growth factor; neurotransmitter.
                                                                                  Prolactin releasing peptide SEQ ID NO:165.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure, Page 244; 733pp; English.
              AAB90991 standard; Peptide; 31 AA.
                                                                                                                                                                                                                                                                        99US-0134406.
99US-0153406.
99US-0159783.
                                                                                                                                                                                                                                                  17-MAY-2000; 2000WO-US13576.
                                                            (first entry)
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                                                                                                                                                                                                                                                                                                                          (CONJ-) CONJUCHEM INC.
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                                                                                                                                                                                                 WO200069900-A2
                                                                                                                                                             Homo sapiens
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15-OCT-1999;
                                                            22-JUN-2001
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                                                                                                                                                                          Synthetic.
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AAB90991
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                                                                                                                                                                                                                                                                                               Human, corticotrophin releasing hormone; CRH; G protein receptor ligand; analgesic; hyperaldosteronism; hypercortisolaemia; hypoadrenocorticism; Addison's disease; adrenal gland hyperfunction; obesity.
 clarifying the physiological functions of the ligand and its derivative. Sequences AAY49290-302 represent peptide fragments of the 19P2 ligand.
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                                                             Length 31;
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                                                                                                                                                                                                                                                                          Human CRH releasing protein related peptide SEQ ID NO: 32.
                                                                                     Indels
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                                                            100.0%; Score 171; DB 21; 100.0%; Pred. No. 5.8e-19;
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                                                                                                                          1 SRTHRHSMEIRTPDINPAWYASRGIRPVGRF 31
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                                                                                                                                                                                                  AAG62531 standard; peptide; 31
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26-SEP-2000; 2000JP-0297073.
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                                                                                                                                                                                                                                                  (first entry)
                                                                                     31; Conservative
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                                                                        Local Similarity
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Thibaudeau K;

Holmes DL,

Milner PG,

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The present invention describes a modified therapeutic peptide (I) comprising a therapeutically active amino acid region (III) and a reactive group (II) (e.g. succinimidyl and maleimido groups) attached to a less therapeutically active amino acid region (IV), which covalently bonds with amino/hydroxyl/thiol groups on blood components to form a peptidase stabilised therapeutic peptide composed of 3-50 amino acids. (I) are useful for modifying therapeutic peptides e.g. hormones, growth actors and neurotransmitters, to protect them from peptidase activity in vivo for the treatment of various disorders. Endogenous therapeutic peptides are not suitable as drug candidates as they require frequent administration due to rapid degradation by peptidases in the body. Modifying and attaching therapeutic peptides to albumin prevents or reduces the action of peptidases to increase length of activity (half Ife and specificity as bonding to large molecules decreases in the ABB90829 to AAB92441 represent peptides which can be used in the exemplification of the present invention.
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100.0%; Pred. No. 5.8e-19;
iive 0; Mismatches 0;
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Best Local Similarity
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1 SRTHRHSMEIRTPDINPAWYASRGIRPVGRF 31

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31; Conservative

Best Local Similarity

RESULT 7

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Homo sapiens.

28-MAR-2002.

Civelli O,

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The invention describes a method of producing a peptide comprising the excision of the N and C-terminals of a target peptide with enzymes or chemically through the attached cleavage sites repeated by ligation in a precursor protein. The method is for producing (low-molecular) peptides e.g. KiSS-1 peptide and GPRB ligand for subsequent applications by the gene recombination technique through tandem repeats to provide a precursor protein with specific cleavage sites. With this method, peptide production can be carried out easily to provide large quantities of the required peptides. This is the amino acid sequence of a peptide associated with the peptide production method of the invention.
                                                                                                                                                                                                                                                                                                                               Process for producing peptides e.g. KiSS-1 peptide and GPR8 ligand for subsequent applications by gene recombination technique through tandem repeats to provide precursor protein with specific cleavage sites -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Process for producing peptides e.g. KiSS-1 peptide and GPR8 ligand for
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100.0%; Pred. No. 5.8e-19;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                              Suenaga M, Ito T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nishimura O, Suenaga M, Ito T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABU60843 standard; Peptide; 31
                                                                                                          16-MAY-2002; 2002WO-JP04735.
                                                                                                                                                      17-MAY-2001; 2001JP-0147341.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-MAY-2002; 2002WO-JP04735.
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                    #0200292829-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to a method of screening for compounds for promoting wakefulness or sleep in a mammal. The method involves administering a prolactin releasing peptide (PrRP) receptor (GRR10) agonist or antagonist respectively and determining the ability of the compound to promote wakefulness or sleep. The compounds identified from the method are used in the therapy of epilepsy and other diseases from the method are used in the therapy of epilepsy and other diseases of sleep. The compounds and narcolepsy. PrRP receptor agonists may be used to treat common disorders which lead to sleepiness, e.g. sleep apnoea, narcolepsy, idiopathic hypersomnia to sleepiness, e.g. sleep apnoea, narcolepsy, idiopathic hypersomnia. PrRP receptor antagonists are useful for promoting sleep and for treating insomnia such as adjustment sleep disorder and psychophysiologic insomnia. The present sequence is the name prRP-31 peptide.
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                                                                                   Human, wakefulness; sleep disorder; prolactin releasing peptide receptor;
PrRP; GPR10; therapy; epilepsy; narcolepsy; sleepiness; sleep apnoea;
insomnia; idiopathic hypersomnia; psychogenic hypersomnia; seizure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Screening for compounds useful for promoting wakefulness or sleep, and for treating sleeping disorders, e.g. insomnia, hypersomnia or sleep apnea, comprises administering a prolactin releasing peptide agonist or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gape
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptide production; low-molecular peptide; KiSS-1; GPR8 ligand; gene recombination.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 31;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 171; DB 23;
100.0%; Pred. No. 5.8e-19;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 SRTHRHSMEIRTPDINPAWYASRGIRPVGRF 31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABU60827 standard; Peptide; 31 AA
                                                                                                                                                                                                                                                                                                                                 17-AUG-2001; 2001US-0932161
                                                                                                                                                                                                                                                                                                                                                                           28-APR-2000; 2000US-0560915
13-DEC-2002 (first entry)
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Best Local Similarity 100.
Matches 31; Conservative
                                       Human PrRP-31 peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-403931/43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lin S;
                                                                                                                                                                                                                                                                                                                                                                                                                     (CIVE/) CIVELLI O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31 AA;
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Homo sapiens

ABU60827;

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Sequence

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Gaps

ö 31;

Length Indels

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                                                                             The invention describes a method of producing a peptide comprising the excision of the N and C-terminals of a target peptide with enzymes or chemically through the attached cleavage sites repeated by ligation in a precursor protein. The method is for producing (low-molecular) peptides e.g. KiSS-1 peptide and GPR8 ligand for subsequent applications by the gene recombination technique through tandem repeats to provide a precursor protein with specific cleavage sites. With this method, peptide production can be carried out easily to provide large quantities of the required peptides. This is the amino acid sequence of a peptide associated with the peptide production method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence represents a peptide fragment from a novel human type ligand polypeptide corresponding to amino acid residues 23 to 54 of the sequence represented in AAW31390 and is used in an assay to monitor ligand binding to the G protein-coupled receptor protein. Pharmaceutical compositions containing this ligand may be used as a pituitary function modulator, a central nervous system modulator or a pancreatic function
subsequent applications by gene recombination technique through tandem repeats to provide precursor protein with specific cleavage sites
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein-coupled receptor; ligand binding; pharmaceutical; odulator; pituitary; central nervous system; pancreas; prophylactic;
                                                                                                                                                                                                                                                                                                                                            Gaps
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in the central nervous system, pancreas and pituitary gland
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                                                                                                                                                                                                                                                                                                          Length 31;
                                                                                                                                                                                                                                                                                                                                          Indels
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                                                                                                                                                                                                                                                                                                       100.0%; Score 171; DB 24;
100.0%; Pred. No. 5.8e-19;
tive 0; Mismatches 0;
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                                                 Disclosure; Page 67; 87pp; Japanese.
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95JP-0343371.
96JP-0059419.
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                                                                                                                                                                                                                                                                                                                        Local Similarity 100.
Les 31; Conservative
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Kawamata Y, Kitada C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 therapeutic agent.
                                                                                                                                                                                                                                                                          31 AA;
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15-MAR-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     modulator;
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                                                                                                                                                                                                                                                                          Sequence
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                                                                                                                                                                                                                                                                                                        Query Match
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modulator. This ligand could have specific applications as a prophylactic or therapeutic agent for dementia, depression, hyperkinetic syndrome, disturbance of consciousness, anxiety syndrome, schizophrenia, trauma, growth hormone secretory disease, hyper- and polyphagia, hyperlipidaemia, hypercholesterolaemia, hyperglyceridaemia, hypercholectinaemia, diabetes, cancer, pancreatitis, renal disease, Turner's syndrome, neurosis, asthma, rheumatoid arthritis, spinal injury, transient brain ischaemia, epilepsy, amylotrophic lateral sclerosis, acute myocardial infarction, infertility, spinocerebellar degeneration, bone fracture, trauma, atopic dermetitis, osteoporosis and/or oligogalactia. Assays can also be developed to screen compounds which are activation of the G protein-coupled receptor protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; oxytocin secretion promoter; G protein-coupled receptor protein; treatment; diseases; pain; atomic bleeding; uterine recovery failure; cow; caesarean section; artificial fertilization; galactostasis; goat; pig; veterinary medicine; milk production.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             which contains a ligand peptide or its salt for the g protein-coupled receptor protein. It is useful in the form of drugs for ameliorating, preventing and treating diseases relating to oxytocin secretion e.g. uterine and atonic bleeding, before and after expulsion of placenta, uterine recovery failure, caesarean section, stoppage of artificial fertilization or galactostasis and is also applicable in veerinary medicine for promoting milk production in cow, goat and pig. This sequence represents a human peptide which acts as an oxytocin secretion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Physiologically-active polypeptide recognized as ligand by G protein-coupled feceptor protein, for promoting secretion of oxytocin, as drugs for diseases relating to oxytocin secretion and in veterinary medicine
                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This invention describes a novel oxytocin secretion-regulating agent
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human oxytocin secretion promoting peptide SEQ ID NO: 33.
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                                                                                                                                                                                                                                                                                                                 100.0%; Score 171; DB 18; 100.0%; Pred. No. 6e-19;
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                                                                                                                                                                                                                                                                                                                                                                                                1 SRITHRHSMEIRTPDINPAWYASRGIRPVGRF 31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                          31, Conservative
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                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 31; Conserv
                                                                                                                                                                                                                                                                              32 AA;
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The invention describes a method of producing a peptide comprising the excision of the N and C-terminals of a target peptide with enzymes or chemically through the attached cleavage after repeated by ligation in a precursor protein. The method is for producing (low-molecular) peptides e.g. KiSS-1 peptide and GPR8 ligand for subsequent applications by the gene recombination technique through tandem repeats to provide a precursor protein with specific cleavage sites With this method, peptide production can be carried out easily to provide large quantities of the required peptides. This is the amino acid sequence of a peptide associated with the peptide production method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Process for producing peptides e.g. KiSS-1 peptide and GPR8 ligand for subsequent applications by gene recombination technique through tandem repeats to provide precursor protein with specific cleavage sites -
                                                                                            Peptide production by gene recombination associated peptide #28
                                                                                                                                   Peptide production, low-molecular peptide, KiSS-1; GPR8 ligand;
gene recombination.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure, Page 67; 87pp; Japanese.
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                                                                                                                                                                                                                                                                                                                  16-MAY-2002; 2002WO-JP04735.
                                                                                                                                                                                                                                                                                                                                                     17-MAY-2001; 2001JP-0147341.
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                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-129302/12.
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                                                                                                                                                                                                                                    WO200292829-A1
                                                                                                                                                                                               Homo sapiens.
                                                         06-MAY-2003
                                                                                                                                                                                                                                                                         21-NOV-2002
                  ABU60844;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                               Human, corticotrophin releasing hormone, CRH; G protein receptor ligand, analgesic; hyperaldosteronism; hypercortisolaemia; hypoadrenocorticism; Addison's disease; adrenal gland hyperfunction; obesity.
                                                                                                Gaps
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                                                         100.0%; Score 171; DB 21; Length 32; 100.0%; Pred. No. 6e-19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Use of G protein receptor ligand or peptide for controlling corticotropin releasing hormone secretion -
                                                                                                                                                                                                                                                                                                                                                                                                Human CRH releasing protein related peptide SEQ ID NO: 33.
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                                                                                                Indels
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                                                                 6e-19,
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100.0%; Pred. No. 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matsumoto H, Hinuma
                                                                                                                                                                                                                                                                           AAG62532 standard; peptide; 32
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26-SEP-2000; 2000JP-0297073.
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                                                                                              Conservative
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                                                                         Local Similarity
es 31; Conserv
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                  32 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200135984-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                     24-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-MAY-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kitada C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                  AAG62532;
                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                         Query Match
                                                                                                                                                                                                                                    RESULT 13
                                                                                              Matches
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Kitada C;

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G protein-coupled receptor; ligand binding; pharmaceutical;
modulator; pituitary; central nervous system; pancreas; prophylactic;
therapeutic agent.
                          Gaps
                          ö
100.0%; Score 171; DB 24; Length 32; 100.0%; Pred. No. 6e-19;
                          Indels
                                                                                                                                                                                                                             Human type G protein-coupled receptor ligand fragment 3.
                          ö
                                                                 SRTHRHSMEIRTPDINPAWYASRGIRPVGRF 31
                                                    1 SRTHRHSMEIRTPDINPAWYASRGIRPVGRF 31
                          0; Mismatches
                                                                                                                                              AAW31393 standard; Peptide; 33 AA
                                                                                                                                                                                                 06-APR-1998 (first entry)
                                                                                                                                                                                                                                                                                                           Homo sapiens
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31

δ 셤 RESULT 14 ABUGO844 ID ABUGO844 standard; Peptide; 32 AA.

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This sequence represents a peptide fragment from a novel human type
ligand polypeptide corresponding to amino acid residues 23 to 55 of the
sequence represented in AAM3139 and is used in an assay to monitor
ligand binding to the G protein-coupled receptor protein. Pharmaceutical
compositions containing this ligand may be used as a pituitary function
modulator, a central nervous system modulator or a pancreatic function
modulator. This ligand could have specific applications as a
modulator or therapeutic agent for dementia, depression, hyperkinetic
prophylactic or therapeutic agent for dementia, depression, hyperlyphactic or therapeutic agent for dementia, depression, hyperlyphactic or therapeutic secrolaemia, hyperlyphagia,
trauma, growth hormone secretory disease, hyper and polyphagia,
hyperlypidaemia, hypercholesterolaemia, hyperlypractideemia,
hyperlypidaemia, hypercholesterolaemia, hyperglyceridaemia,
hyperprolactinaemia, diabetes, cancer, pancreatitis, renal disease,
hyperprolactinaemia, epilepsy, amylotrophic lateral sclerosis,
cute myocardial infarction, infertility, spinocerebellar degeneration,
cute myocardial infarction, infertility, spinocerebellar degeneration,
coute myocardial infarction, infertility, spinocerebellar degeneration,
coligogalactia Assays can alloo be developed to screen compounds which are
capable of altering the binding activity of the ligand affecting
activation of the G protein-coupled receptor protein.
                                                                                                                                                                                                                                                                                                                                                                                Ligand peptide for G protein-coupled receptor - acts by modulating function in the central nervous system, pancreas and pituitary gland
                                                                                                                                                                                                                                    Pujii R, Fukusumi S, Habata Y, Hinuma S, Hosoya M;
Kawamata Y, Kitada C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 2; Page 185; 258pp; English.
                                                                                             95JP-0343371.
96JP-0059419.
96JP-0211805.
                        96WO-JP03821.
                                                                       96JP-0246573
                                                                                                                                                                                        (TAKE ) TAKEDA CHEM IND LTD
                                                                                                                                                                                                                                                                                                           WPI; 1997-363672/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 33 AA;
                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAV02430
                        26-DEC-1996;
                                                                                               28-DEC-1995;
15-MAR-1996;
                                                                    18-SEP-1996;
                                                                                                                                         12-AUG-1996;
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Search completed: December 3, 2003, 19:11:24 Job time : 33.75 secs

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Gaps

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/ Match 100.0%; Score 171; DB 18; Length 33; Local Similarity 100.0%; Pred. No. 6.3e-19; No. 6.3e-19; No. 8.31; Conservative 0; Mismatches 0; Indels 0

Query Match Best Loc Matches 1 SRTHRHSMEIRTPDINPAWYASRGIRPVGRF 31 SRTHRHSMEIRTPDINPAWYASRGIRPVGRP

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122, App
136, App
136, App
115, App
117, App
117, App
137, Appl
47, Appl
47, Appl
8, Appl
137, Appl
137, Appl
14, Appl
14, Appl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 9, Application US/09105678A

Fatent No. 6103882
GENERAL INFORMATION:
APPLICANT: Suenaga, Masato
APPLICANT: Suenaga, Masato
APPLICANT: Tanaka, Yoko
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
ITILE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPOURE: IBM PC compatible
COMPOURE: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,678A
PILING DATE: 26-JUN-1998
PRIOR PALICATION NUMBER: UP 172118/1997
PILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: COMIN, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48466-342
TELECOMMULICATION INFORMATION:
TELECOMMULICATION INFORMATION:
TELECOMMULICATION INFORMATION:
TELECOMMULICATION INFORMATION:
TELECOMMULICATION INFORMATION:
TELECOMMULICATION INFORMATION:
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100.0%; Pred. No. 7.3e-19;
tive 0; Mismatches 0;
                                   US-08-776-971-44

US-08-776-971-122

US-08-776-971-131

US-08-776-971-115

US-08-776-971-115

US-09-776-971-117

US-09-105-678A-8

US-09-105-678A-8

US-09-105-678A-9

US-09-105-678-9

US-09-105-678-9
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US-08-776-971-48
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                                                                                                                                                                                                                                                                                                                                                                                                                             ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 100.
Matches 31; Conservative
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MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-105-678A-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-105-678A-9
Query Match
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7, App
31, App
31, Appli
5, Appli
7, Appli
7, Appli
31, Appli
13, Appli
6, Appli
6, Appli
6, Appli
6, Appli
                                                                                                                                       December 3, 2003, 19:09:05; Search time 11.5 Seconds (without alignments) 114.055 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 15,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence Seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence Sequence Sequence Sequence
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Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Issued Patents AA:*

(cgn2_6/ptodata/1/laa/5A_COMB.pep:*

(cgn2_6/ptodata/1/laa/5B_COMB.pep:*

(cgn2_6/ptodata/1/laa/6A_COMB.pep:*

(cgn2_6/ptodata/1/laa/6B_COMB.pep:*

(cgn2_6/ptodata/1/laa/PcTUS_COMB.pep:*

(cgn2_6/ptodata/1/laa/PcTUS_COMB.pep:*
                 GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                    171
1 SRTHRHSMEIRTPDINPAWYASRGIRPVGRF 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-105-678A-9
US-09-105-678A-43
US-09-421-208-9
US-09-421-208-9
US-09-421-208-9
US-09-421-208-9
US-09-421-208-44
US-09-105-678A-45
US-09-105-678A-45
US-09-105-678A-45
US-09-105-678A-45
US-09-105-678A-45
US-09-105-678A-138
US-09-105-678A-3
                                                                                                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                 328717 seqs, 42310858 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                      OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                US-09-868-885B-32
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100.0
100.0
92.4
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                                                                                                                                                                                                                              Title:
Perfect score:
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                                                                                                                                                                                                                                                                             Sequence:
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BRONSTEIN, ROBERTS & CUSHMAN, LLP
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| Patent No. 6258561
| GENERAL INFORMATION:
| GENERAL INFORMATION:
| APPLICANT: Moriya, Takeo
| APPLICANT: Tanaka, Yoko
| APPLICANT: Tanaka, Yoko
| APPLICANT: Nishimura Osamu
| TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
| NUMBER OF SEQUENCES: 52
| NUMBER OF SEQUENCES: 52
| CORRESPONDENCE ADDRESS: 53
| ADDRESSER: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                CURRENT ITES: LERACEDE
COMBUTER: IEM COMPACTIOE
CORRENTING SYSTEM: DOS
SOFTWARE: PASTEM: DOS
SOFTWARE: PASTEM: DOS
SOFTWARE: PASTEM: DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06-Feb-1997
CLASSIFTCATION DATA:
APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: JP 7/343371
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: JP 8/59419
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: JP 8/59419
FILING DATE: 12-AUG-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-AUG-1996
APPLICATION NUMBER: JP 8/21605
FILING DATE: 12-AUG-1996
APPLICATION NUMBER: JP 8/216573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             B: DIKE, BRONSTEIN, ROBERTS & CUSHWAN, LLP
130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
100.0%; Score 171; DB 3;
Best Local Similarity 100.0%; Pred. No. 7.3e-19;
Matches 31; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 SRITHRHSMEIRTPDINPAWYASRGIRPVGRF 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 SRTHRHSMEIRTPDINPAWYASRGIRPVGRF 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | LENGTH: 31 amino acids | TYPE: amino acids | TYPE: amino acids | TYPE: amino acid | STRANDEDNESS: aingle | TOPOLOGY: linear | MOLECULE TYPE: protein | FRAGENT TYPE: internal | SEQUENCE DESCRIPTION: SEQ ID NO: 61: US-08-776-971-61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY AGENT INFORMATION:
NAME: Conlin, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 47176
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEPAX: 617-523-3400
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
                 STREET: 130 Water Street
                                                                                                                   ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
  ADDRESSEE: DIKE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                               USA
                                                   CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JS-09-421-208-9
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Kawamata, Yuji
Hosoya, Masaki
Fujii, Ryo
Fukusumi, Shoji
Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 171; DB 3; Length 31; 100.0%; Pred. No. 7.3e-19; tive 0; Mismatches 0; Indels
                                                                                                                                    Sequence 43, Application US/09105678A

Patent No. 6103892
GENERAL INPORMATION:
GENERAL INPORMATION:
APPLICANT: Standad, Masato
APPLICANT: Tandad, Yoko
APPLICANT: Tandad, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: RIOPPY disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPANIOS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,678A
PILING DATE: 26-JUN 1999
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 172118/1997
ATTORNEY/AGENT INFORMATION:
SRITHRHSMBIRTPDINPAWYASRGIRPVGRF 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 SRTHRHSMEIRTPDINPAWYASRGIRPVGRF 31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 61, Application US/08776971B
Patent No. 6228984
GENERAL INFORMATION:
APPLICANT: Hinuma, Shuji
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Conlin, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 4846
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-540
TELEFAX: 617-523-6440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100...
Best 31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; MOLECULE TYPE: peptide US-09-105-678A-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
                                                                                                                                                                                                                                                                                                                                                                                                                                 Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: MA
COUNTRY: U
                                                                                                  RESULT 2
US-09-105-678A-43
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WS-09-560-915-15

### Sequence 15, Application US/09560915

### Sequence 15, Application US/09560915

#### Sequence 15, Application US/09560915

#### Sequence 15, Application US/09560915

### Sequence 15, Application US/09560915

#### Septicant: Civelli, Olivier

### APPLICANT: Civelli, Olivier

### Septicant: Civelli, Olivier

### TITLE OF INVENTION: Therapeutic Compositions and Methods

### TITLE OF INVENTION: Therapeutic Compositions and Methods

### TITLE OF INVENTION: Relating To Prolactin Releasing Peptide (PrRP)

### TITLE OF INVENTION: Relating To Prolactin Releasing Peptide (PrRP)

### CURRENT APPLICATION NUMBER: 2000-04-28

### CURRENT PRING DATE: 2000-04-28

### SOFTWARE: PastSEQ for Windows Version 4.0

### SEQ ID NO 15

### ILENGTH: 31

### TYPE: RPT

### CRANISM: Homo Sapien

US-09-560-915-15
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                                                                                                                                                                                                                                                                                  Query Match 100.0%; Score 171; DB 3; Length 31; Best Local Similarity 100.0%; Pred. No. 7.3e-19; Matches 31; Conservative 0; Mismatches 0; Indels
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APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Moriya, Takeo
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,678A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 171; DB 4;
100.0%; Pred. No. 7.3e-19;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                              1 SRITHRHSMEIRTPDINPAWYASRGIRPVGRF 31
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                                                              43:
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                                                                                                             i LENGTH: 31 amino acids
rypR: amino acid
rypR: amino acid
rypR: amino acid
rypR: roPOLOGY:
roPOLOGY: linear
roPOLOGY: linear
ropology: linear
ropology: linear
ropology: linear
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Matches 31; Conservative
                                    TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
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STATE: MA
COUNTRY: US
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US-09-105-678A-44
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APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CUSHMAN, LLP STREET: 130 Water Street
CITY: Boeton
STREET: ASSETS STREET
CITY: Boeton
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/421,208
PILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/421,208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
100.0%; Score 171; DB 3;
Best Local Similarity 100.0%; Pred. No. 7.3e-19;
Matches 31; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SRITHRHSMEIRIPDINPAMYASRGIRPVGRF 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 SRIHRHSMEIRIPDINPAWYASRGIRPVGRF 31
                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/105,678
FILING DATE: 25-JUN-1998
APPLICATION NUMBER: UP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: COALIN, David G.
REGISTRATION NUMBER: 27,026
REGISTRATION NUMBER: 27,026
REGISTRATION NUMBER: 48466-342
TELEPONE: 617-523-400
TELEPAX: 617-523-440
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE GHARACTERISTICS:
LENGTH: 31 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/105,678
FILING DATE: 26-UNN-1998
APPLICATION NUMBER: UP 172118/1997
FILING DATE: 27-UNN-1997
ATORNEY/AGENT INFORMATION:
NAME: CONLIN, DAYIG G.
REGISTRATION NUMBER: 27,026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 48466-342
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 5
US-09-421-208-43
Sequence 43, Application US/09421208
; Patent No. 625851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-421-208-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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Pred. No. 7.6e-19;
                                                                                                                                                                                                                                                                                                                                        Length 32;
                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 44, Application US/09421208
Patent No. 6258561
GENERAL INFORMATION:
APPLICANT: Suenaga, Masato
APPLICANT: Moritya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Niblimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 'LIGAND
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/421,208
                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.0%; Pred. No. 7.6e-19;
Matches 31; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 SRITHRHSMEIRTPDINPAWYASRGIRPVGRF 31
                                                                                                                                              TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
NOLECULE TYPE: protein
FRACHENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 62:
US-08-776-971-62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 09/105,678
FILING DATE: 26-UN-1998
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATYORNEY/AGENT INFORMATION:
NAME: CONLIN, David G-
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48466-342
TELECHONNICATION INFORMATION:
TELECHONE: 617-523-3400
TELEFRAX: 617-523-3400
REPERENCE/DOCKET NUMBER: 47176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                TELECOMOUNICATION INFORMATION
TELEPHONE: 617-523-3400
TELEPAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%;
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CITY: Boston
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
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Kawamata, Yuji
Hosoya, Maski
Fujii, Ryo
Fukusumi, Shoji
Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
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ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: 1BM compatible

COWFUTER: 1BM compatible

COWFUTER: 1BM compatible

OPERATING SYSTEM: DOS

SOFTWARE: PASESEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/776,971B

FILING DATE: 06-Feb-1997

CLASSIFICATION OFFED-1997

RILING DATE: 28-DEC-1996

APPLICATION NUMBER: JP 9/34331

FILING DATE: 28-DEC-1996

APPLICATION NUMBER: JP 8/5919

FILING DATE: 15-MAR-196

APPLICATION NUMBER: JP 8/211805

FILING DATE: 12-AUG-1996

APPLICATION NUMBER: JP 8/21805

FILING DATE: 12-AUG-1996

APPLICATION NUMBER: JP 8/21605

FILING DATE: 12-AUG-1996

APPLICATION NUMBER: JP 8/246573
                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 171; DB 3; 100.0%; Pred. No. 7.6e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SRITHRHSMEIRIPDINPAWYASRGIRPVGRF 31
                PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUL-1997
ATTORNEY/AERY INFORMATION:
NAME: Conlin, David G.
REGISTRATION NUMBER: 27,026
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48466-342
TELEPHONE: 617-523-3400
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Conlin, David G.
REGISTRATION NUMBER: 27,026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 62, Application US/08776971B Patent No. 6228984 GENERAL INFORMATION:
                                                                                                                                                                                                                          TELEFAX: 617-523-6440

INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
COS-105-678A-44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Hinuma, Shuji
Habata, Yugo
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 100.
Best Local Similarity 100.
Matches 31; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Boston
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Gaps
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 33
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Sequence 45, Application US/09421208
Sequence 45, Application US/09421208
Sequence 40 Moniya, Takeo
APPLICANT: Moniya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
MUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                      MEDLUM TYPE: IBM Compatible
CORRUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastESEQ for Windows Version 2.0
CURRNT APPLICATION DATA:
APPLICATION NUABER: US/08/776,971B
FILING DATE: 06-Feb-1997
CLASSIPICATION ATA:
APPLICATION ATA:
APPLICATION DATA:
APPLICATION NUMBER: DT /34331
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: JP 9/34331
FILING DATE: 18-DEC-1996
APPLICATION NUMBER: JP 8/59419
FILING DATE: 12-AUG-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-AUG-1996
APPLICATION NUMBER: JP 8/211805
APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: CONIIN: DAVIG G.
REGISTRATION NUMBER: 27,026
REGISTRATION NUMBER: 27,026
TELECOMMUNICATION HUMBER: 27,026
TELECOMMUNICATION HUMBER: 47176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, STREET: 130 Water Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.0%; Score 171; DB 3; Best Local Similarity 100.0%; Pred. No. 7.9e-19; Matches 31; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 SRTHRHSMBIRTPDINPAWYASRGIRPVGRF 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 SRTHRHSMBIRTPDINPAWYASRGIRPVGRF 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
FRACHENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 63:
US-08-776-971-63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: 617-523-3400
TELEFAX: 617-523-640
INFORMATION FOR SEQ. ID NO: 63:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                              ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
                                                                                                                                                                        USA
                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 12
US-09-421-208-45
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              Gaps
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                                                                                                                                                                                              Sequence 45. Application US/09105678A
; Sequence 45. Application US/09105678A
; Patent No. 6103882
; GENERAL INFORMATION:
    APPLICANT: Suenaga, Masato
    APPLICANT: Analya, Takeo
    APPLICANT: Nishimura, Osamu
    APPLICANT: Nishimura, Osamu
    TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
    NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESSE:
    ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
    STREET: 130 Water Street
    CONTY: Boston
              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE: 26-JUN 1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/105,678A

FILING DATE: 27-JUN-1997

ATTORNEY/AGENT INFORMATION:

NAME: Conlin, David G.

REFERENCE/POCKET NUMBER: 48466-342

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-523-3400

TELEPHONE: 617-523-640

INFORMATION FOR SEQ ID NO: 45:

SEQUENCE CHARACTERISTICS:
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                                                                                    1 SRTHRHSMEIRTPDINPAWYASRGIRPVGRF 31
         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Kawamata, Yuji
Hosoya, Masaki
Fujii, Ryo
Fukusumi, Shoji
Kitada, Chieko
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 33 amino acida
         31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
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US-09-105-678A-45
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US-08-776-971-63
         Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEB: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP STREET: 130 Water Street CITY: Boston STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 87;
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COMPUTER RRADBELE FORM:
MEDIUM TYPE: Diskette
COMPUTER: 1BM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION AUMBER: US/08/776,971B
FILING DATE: 06-Feb-1997
CLASSIFICATION: «Unknown»
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 171; DB 3;
Pred. No. 2.4e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP96/03821
PILING DATE: 28-DEC-1996
APPLICATION NUMBER: JP 7/34331
PILING DATE: 28-DEC-1995
APPLICATION NUMBER: JP 8/59419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 SRITHRHSMBIRIPDINPAWYASRGIRPVGRF 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23 SRTHRHSMEIRTPDINPAWYASRGIRPVGRF 53
                             FILING DATE: 15-WAR-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-AUG-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: 10-82F-1996
ATORNEY/AGENT INFORMATION:
NAME: CONJIN, DAVIG G.
REGISTRATION NUMBER: 27,026
REPERENCE/DOCKET NUMBER: 47176
TELECOMMUNICATION INPORMATION:
TELEFRAK: 617-523-3400
TELEFRAK: 617-523-6440
INPORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: JP 8/211805
                                                                                                                                                                                                                                                                                                                                                  MOLECULA TYPE: protein FRACHENT TYPE: Internal SEQUENCE DESCRIPTION: SEQ ID NO: 59: US-08-776-971-59
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: JP 8/59419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 135, Application US/08776971B Patent No. 6228984 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 12-AUG-1996
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Hosoya, Masaki
Fujii, Ryo
Fukusumi, Shoji
Kitada, Chieko
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                                                                                                                                                                                                                                                                                     LENGTH: 87 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%;
                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Hinuma, Shuji
Habata, Yugo
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Best Local Similarity 100.
Matches 31, Conservative
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TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 33;
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CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COURTER: IEM COMPATIBLE
COMPUTER: IEM COMPATIBLE
COPERATING SYSTEM: DOS
SOFTWARE: FASTEM: DOS
SOFTWARE: FASTEM: DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06-Feb-1997
CLASSIFICATION CONFRONT
APPLICATION NUMBER: PCT/JP96/03821
FILING DATE: 28-DEC-1996
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: JP 7/343371
                                              Query Match
100.0%; Score 171; DB 3;
Best Local Similarity 100.0%; Pred. No. 7.9e-19;
Matches 31; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SRITHRHSMEIRTPDINPAWYASRGIRPVGRF 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SRITHRHSMEIRTPDINPAWYASRGIRPVGRF 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 59, Application US/08776971B Patent No. 6228984 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kawamata, Yuji
Hosoya, Masaki
Fujii, Ryo
Fukusumi, Shoji
                                   B: Ploppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Hinuma, Shuji
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-421-208-45
                  COMPUTER READABLE FORM: MEDIUM TYPE: Ploppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Habata,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 13
US-08-776-971-59
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KAWAMALA, Yuji
Hosoya, Masaki
Fujii, Ryo
Fujii, Ryo
Fujii, Ryo
Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS:
ADDRESSE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FREEEG for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06-Feb-1997
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: PCT/JP96/03821
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: JP 7/343371
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: JP 8/5919
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-AUG-1996
APPLICATION NUMBER: JP 8/21605
FILING DATE: 12-AUG-1996
APPLICATION NUMBER: JP 8/216573
FILING DATE: 12-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 171; DB 3;
Pred. No. 2.4e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 SRITHRHSMEIRTPDINPAWYASRGIRPVGRF 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23 SRTHRHSMEIRTPDINPAWYASRGIRPVGRF 53
APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: CONLIA, DAVIG G.
REGISTRATION NUMBER: 27,026
REGISTRATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPRACE 617-523-3400
INFORMATION FOR SEQ ID NO: 135:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear

MOLECULE TYPE: protein

PRAGMENT TYPE: internal

SEQUENCE DESCRIPTION: SEQ ID NO: 135:
US-08-776-971-135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Conlin, David G.
REGISTRATION NUMBER: 27,026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 138, Application US/08776971B
Patent No. 6228984
GENERAL INFORMATION:
APPLICANT: Hinuma, Shuji
Habata, Yugo
                                                                                                                                                                                                                                                           LENGTH: 87 amino acida
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.0%;
Matches 31; Conservative 0
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TYPE: PRT
CORGANISM: Homo Sapien
US-09-932-161-15
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                                                                                                                                   December 3, 2003, 19:11:30 ; Search time 22.5 Seconds (without alignments) 256.244 Million cell updates/sec
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Sequence 88,
Sequence 14,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Published Applications AA:*

1: \cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

2: \cgn2_6/ptodata/1/pubpaa/PCT_RMF PUB.pep:*

3: \cgn2_6/ptodata/1/pubpaa/PCT_RMF PUB.pep:*

4: \cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

5: \cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

6: \cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*

7: \cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*

8: \cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*

9: \cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*

10: \cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*

11: \cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*

11: \cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*

12: \cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*

13: \cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*

14: \cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*

15: \cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*

15: \cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*

17: \cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*

18: \cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*

18: \cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
               GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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171
1 SRTHRHSMEIRTPDINPAWYASRGIRPVGRF 31
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US-10-096-777-15
US-10-096-777-15
US-09-932-161-13
US-10-096-777-13
US-10-096-777-13
US-10-044-592-39
US-10-044-592-38
US-10-044-592-38
US-10-044-592-38
US-10-044-592-38
US-10-044-592-38
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                                                                                                                                                                                                                                                                                                                                                                            684280 seqs, 185983659 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                  - protein search, using sw model
                                                                                                                                                                                                                                                                                                               BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Match Length
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Sequence 11, Appli
Sequence 14, Appli
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Sequence 18, Appl
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Sequence 15, Application US/09932161

SERNEAL INFORMATION:

SERVELL INFORMATION:

APPLICANT: Civelli, Olivier

TITLE OF INVENTION: Screening and Therapeutic Methods For INVENTION: Promoting Wakefulness and Sleep

FILE REFERRANCE: PUC 4679

CURRENT FILING DATE: 2001-08-17

PRIOR APPLICATION NUMBER: US/09/932,161

WUMBER OF SEQ ID NOS: 24

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 15

LENGTH: 31
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4 US-10-096-777-14

4 US-10-044-592-4

4 US-10-044-592-90

4 US-10-044-592-90

4 US-10-044-592-96

4 US-10-044-592-94

4 US-10-044-592-94

4 US-10-044-592-78

US-09-932-161-18

US-09-932-161-16

US-09-932-161-16

US-09-932-161-16

US-10-044-592-42

US-10-044-592-44

US-10-044-592-6

4 US-10-044-592-6

4 US-10-044-592-6

4 US-10-044-592-6

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US-10-104-592-80
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US-10-096-777-15
; Sequence 15, Application US/10096777
; Publication No. US20030171270A1
; GRURRAL INFORMATION:
; APPLICANT: Civelli, Olivier
; APPLICANT: Lin, Steven
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Sequence 13, Application US/10096777

Publication No. US20030171270A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Civelli, Olivier
ITILE OF INVENTION: Therapeutic Compositions and Methods
ITILE OF INVENTION: Therapeutic Compositions and Methods
ITILE OF INVENTION: Relating To Prolactin Releasing Peptide (PIRP)
FILE REFERENCE: P-UC 3534

CURRENT APPLICATION NUMBER: US/10/096,777

CURRENT PILIG DATE: 2002-03-12

PRIOR PILIGATION NUMBER: US/09/560,915

PRIOR FILING DATE: 2000-04-28

NUMBER OF SEQ ID NOS: 24

SOFTWARE: PASESEQ for Windows Version 4.0

SEQ ID NO 13

LENGTH: 21
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Sequence 39, Application US/10044592

Publication No. US20020143152A1

GENERAL INPORMATION:

APPLICANT: Hinuma, Shuji

APPLICANT: Hinuma, Shuji

TITLE OP INVENTION: Polypeptides, their Production and Use

FILE REPERROR: 2463US2P

CURRENT FILING DATE: 2002-01-10

PRIOR PELICATION NUMBER: US/10/044,592

CURRENT FILING DATE: 1999-25-10

PRIOR PELICATION NUMBER: US/10/98/01923

PRIOR PELICATION NUMBER: PCT/JP98/01923

PRIOR PELICATION NUMBER: PCT/JP98/01923

PRIOR PILING DATE: 1999-04-28

NUMBER OF SEQ ID NOS: 96

LENGTH: 31

TYPE: PRT

TYPE: 
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Pred. No. 8.5e-16;
1; Mismatches 2; Indels
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SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 13 LENGTH: 31
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Best Local Similarity 90.3%;
Matches 28; Conservative
                                                                                                                                                                                                                                      Query Match
Best Local Similarity 90.33
Matches 28; Conservative
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CRGANISM: Bos taurus
US-10-096-777-13
                                                                                                       t TYPE: PRT
COGANISM: BOS taurus
US-09-932-161-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-044-592-39
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US-10-096-777-13
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TITLE OF INVENTION: Therapeutic Compositions and Methods
TITLE OF INVENTION: Relating TO Prolactin Releasing Peptide (PRRP)
FILE REFERENCE: P-UC 3534
CURRENT APPLICATION NUMBER: US/10/096,777
CURRENT FILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: US/09/560,915
PRIOR FILING DATE: 2000-04-28
NUMBER OF SEQ ID NOS: 24
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 15
LENGTH: 31
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Sequence 92, Application US/10044592
Publication No. US20020143152A1
GENERAL INFORMATION:
APPLICANT: Hinuma, Shuji
TITLE OF INVENTION: POLYPEPTIGES, their Production and Use
FILE REPERENCE: 2463US2P
CURRENT APPLICATION NUMBER: US/10/044,592
CURRENT FILING DATE: 1099-25-10
PRIOR PLICATION NUMBER: DCT/JP98/01923
PRIOR FILING DATE: 1999-25-10
PRIOR FILING DATE: 1999-25-10
PRIOR PLING DATE: 1999-25-10
PRIOR PLING DATE: 1999-25-10
PRIOR FILING DATE: 1999-64-27
PRIOR FILING DATE: 1999-64-28
NUMBER OF SEQ ID NOS: 96
SEQ ID NO 92
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Patent No. US20020037533A1
GENERAL INFORMATION:
APPLICANT: Civelli, Olivier
APPLICANT: Lin, Steven
TITLE OF INVENTION: Promoting Wakefulness and Sleep
TITLE OF INVENTION: Promoting Wakefulness and Sleep
FILE REPERENCE: PuC 4679
CURRENT FILING DATE: 2001-08-17
PRIOR APPLICATION NUMBER: US 09/560,915
PRIOR PILLING DATE: 2000-04-28
NUMBER OF SEQ ID NOS: 24
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100.0%; Pred. No. 1.1e-17;
iive 0; Mismatches 0;
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Matches 31; Conservative
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US-10-044-592-92
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ORGANISM: Homo Sapien
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US-10-044-592-92
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Sequence 38, Application US/10044592

Sequence 38, Application US/10044592

Publication No. US20020143152A1

GENERAL INFORMATION:

APPLICANT: Hinuma, Shuji

TITLE OF INVENTION: Polypeptides, their Production and Use

FILE REPERENCE: 2463US2P

CURRENT PILING DATE: 2002-01-10

PRIOR PILING DATE: 1999-25-10

PRIOR PLING DATE: 1999-25-10

PRIOR APPLICATION NUMBER: PCT/JP98/01923

PRIOR PLING DATE: 1999-04-27

PRIOR APPLICATION NUMBER: PCT/JP98/01923

PRIOR PLING DATE: 1997-04-28

NUMBER OF SEQ ID NOS: 96

SOFTWARE:

SEQ ID NO 38

LENGTH: 98
                                                                                                                                                                             APPLICANT: Hinuma, Shuji
APPLICANT: Hinuma, Shuji
APPLICANT: Fukusuumi, Shoji
TITLE OF INVENTION: Polypeptides, their Production and Use
FILE REPRENCE: 2463U32P
CURRENT APPLICATION NUMBER: US/10/044,592
CURRENT FILING DATE: 2002-01-10
PRIOR APPLICATION NUMBER: US 09/403639
PRIOR PILING DATE: 1999-25-10
PRIOR FILING DATE: 1999-64-27
PRIOR FILING DATE: 1998-64-27
PRIOR FILING DATE: 1998-64-27
PRIOR FILING DATE: 1997-04-28
NUMBER OF SEQ ID NOS: 96
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Pred. No. 2.8e-15;
1; Mismatches 2;
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1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRP 31
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Sequence 28, Application US/10044592
Publication No. US/2020143152A1
GENERAL INFORMATION:
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Best Local Similarity 90.3%;
Matches 28; Conservative 1
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Best Local Similarity
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; ORGANISM: Bovine
US-10-044-592-38
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ORGANISM: Murine
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Sequence 41, Application US/10044592

Publication No. US20020143152A1

GRERAL INFORMATION:

APPLICANT: Hinuma, Shuji

APPLICANT: Fukusumi, Shoji

ITLE OF INVENTION: Polypeptides, their Production and Use

FILE REFERENCE: 2463US2P

CURRENT FILING DATE: 2002-01-10

FRIOR APPLICATION NUMBER: US/10/044,592

CURRENT FILING DATE: 1999-25-10

PRIOR PILING DATE: 1999-25-10

PRIOR APPLICATION NUMBER: PCT/JP98/01923

PRIOR PILING DATE: 1999-04-27

PRIOR APPLICATION NUMBER: JP 9-109974

PRIOR FILING DATE: 1999-04-28

NUMBER OF SEQ ID NOS: 96

SOFTWARE:

SEP TR. 100
                                                                                                                                                                                                                                                                                               APPLICANT: Hinuma, Shuji
APPLICANT: Hinuma, Shuji
APPLICANT: Fukusumi, Shoji
ITILE OF INVENTION: Polympetides, their Production and Use
FILE REPERENCE: 46510S2P
CURRENT APPLICATION NUMBER: US/10/044,592
CURRENT PILING DATE: 2002-01-10
PRIOR PILING DATE: 1999-25-10
PRIOR PILING DATE: 1999-04-27
PRIOR PILING DATE: 1999-04-28
PRIOR PILING DATE: 1999-04-28
NUMBER: OF SEQ ID NOS: 96
SOFTWARE: SOFTWARE: 1900-04-28
SOFTWARE: 1000-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 92.4%; Score 158; DB 14; Length 32; Best Local Similarity 90.3%; Pred. No. 8.8e-16; Matches 28; Conservative 1; Mismatches 2; Indels
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  Similarity 90.3%; Pred. No. 8.5e-16; 28; Conservative 1; Mismatches 2; Indels
                                                                                                 1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31
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                                                                      1 SRTHRHSMEIRTPDINPAWYASRGIRPVGRF 31
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; Sequence 40, Application US/10044592
; Publication No. US20020143152A1
; GENERAL INFORMATION:
Best Local Similarity
Matches 28; Conserv
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; ORGANISM: Bovine
US-10-044-592-41
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LENGTH: 33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92.4%; Score 158; DB 14; Length 98; 90.3%; Pred. No. 2.8e-15; live 1; Mismatches 2; Indels
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                 TITLE OF INVENTION: Polypeptides, their Production and Use
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Patent No. US20020037533A1
GENERAL INFORMATION:
APPLICANT: Lin, Steven
TITLE OF INVENTION: Screening and Therapeutic Methods For TITLE OF INVENTION: Promoting Wakefulness and Sleep FILE REFERENCE: P-UC 4679
CURRENT APPLICATION NUMBER: US/09/932,161
CURRENT FILING DATE: 2001-08-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 92.4%; Score 158; DB 14;
Best Local Similarity 90.3%; Pred. No. 2.8e-15;
Matches 28; Conservative 1; Mismatches 2;
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                                         FILE REPERENCE: 2463US2P;
CURRENT APPLICATION NUMBER: US/10/044,592
CURRENT FILING DATE: 2002-01-10
PRIOR APPLICATION NUMBER: US 09/403639
PRIOR PILING DATE: 1999-25-10
PRIOR PILING DATE: 1999-04-27
PRIOR PILING DATE: 1998-04-27
PRIOR PILING DATE: 1998-04-27
PRIOR PILING DATE: 1997-04-28
NUMBER OF SEQ ID NOS: 96
SQPTWARE:
SQPTWARE:
SQPTWARE:
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, ORGANISM: Bovine
US-10-044-592-86
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ORGANISM: Bovine
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US-09-932-161-14
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Sequence 82, Application US/10044592

Publication No. US20020143152A1

GENERAL INPORMATION:

APPLICANT: Hinuma, Shuji

TITLE OF INVENTION: Polypeptides, their Production and Use
FILER REPERENCE: 24631052P

CURRENT APPLICATION NUMBER: US/10/044,592

CURRENT APPLICATION NUMBER: US/10/044,592

CURRENT APPLICATION NUMBER: US/10/044,592

PRIOR PILING DATE: 1999-25-10

PRIOR APPLICATION NUMBER: PCT/JP98/01923

PRIOR PILING DATE: 1999-04-27

PRIOR PILING DATE: 1999-04-27

PRIOR FILING DATE: 1997-04-28

NUMBER OF SEQ ID NOS: 96
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APPLICANT: Fukusumi, Shoji
TITILE OF INVENTION: Polypeptides, their Production and Use;
TITLE OF INVENTION: Polypeptides, their Production and Use;
FILE REFERENCE: 4563US2P
CURRENT APPLICATION NUMBER: US/10/044,592
CURRENT FILING DATE: 1999-25-10
PRIOR APPLICATION NUMBER: PCT/JP99/01923
PRIOR PILING DATE: 1998-64-27
PRIOR PLING DATE: 1998-64-27
PRIOR PLING DATE: 1998-64-27
PRIOR PLING DATE: 1998-64-27
PRIOR PLING DATE: 1998-64-27
SROR FILING DATE: 1998-64-28
NUMBER OF SEQ ID NOS: 96
SSEQ ID NO 84
LENGTH: 98
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90.3%; Pred. No. 2.8e-15;
live 1; Mismatches 2;
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Sequence 86, Application US/10044592

Publication No. US20020143152A1

GENERAL INFORMATION

APPLICANT: Hinnma, Shuji

APPLICANT: Fukusumi, Shoji
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Best Local Similarity 90.3
Matches 28; Conservative
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Matches 28; Conservative
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ORGANISM: Bovine
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ORGANISM: Bovine
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US-10-044-592-84
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LENGTH: 98
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; PRIOR APPLICATION NUMBER: US 09/560,915; PRIOR FILING DATE: 2000-04-28; NUMBER: OF SEQ ID NOS: 24; SEQ ID NO 14; SEQ ID NO 14; LENGTH: 31; TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT US-09-932-161-14
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Search completed: December 3, 2003, 19:17:37 Job time : 22.5 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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- protein search, using sw model OM protein Run on:

December 3, 2003, 19:05:30 ; Search time 10.5 Seconds (without alignments) 283.927 Million cell updates/sec

US-09-868-885B-32 171 Title: Perfect score:

1 SRTHRHSMEIRTPDINPAWYASRGIRPVGRF 31 Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters:

283308 seqs, 96168682 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR 76:*
1: pirl:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

					SUMMARIES	
Result		Query				
No.	Score	Match	Length	8	QI	Description
-	149	87.1	83	8	JC7607	prolactin-releasin
7	56.5	33.0		N	F83376	conserved hypothet
e	54	31.6		~	T47959	hypothetical prote
4	53.5	31.3		~	B70569	hypothetical prote
S	53	31.0		~	D87559	sensory box histid
9	52	30.4		~	F69099	sensory transducti
7	50.5	29.5	1882	~	S73484	
80	20	29.5		~	S77900	
6	20	29.5		N	S76955	
10	49.5	28.9		N	867150	hypothetical prote
11	49	28.7		7	B91002	probable regulator
12	48.5	28.4		N	AH2016	hypothetical prote
13	48.5	28.4		N	T45623	hypothetical prote
14	48	28.1	118	~	AC3169	hypothetical prote
15	48	28.1		N	C83292	probable glutathio
16	48	28.1		~	S70671	lipopolysaccharide
17	48	28.1		~	T21648	hypothetical prote
18	48	28.1		N	D70885	probable aldC prot
19	48	28.1		~	T33759	hypothetical prote
20	47.5	27.8		~	D84012	N-acetylglutamate
21	47.5	27.8		N	AB2664	conserved hypothet
22	47.5	27.8		~	A97446	hypothetical prote
23	47.5	27.8		~	A82193	Sun/nucleolar prot
24	47.5	27.8		N	A33111	segmentation prote
25	47	27.5		N	G82669	ubiquinone biosynt
56	47	27.5	215	~	B87577	glutathione S-tran
27	47	27.5		7	F71015	hypothetical prote
78	47	27.5	333	ų	H82852	ಹ
53	47	27.5	501	N	T48336	hypothetical prote

hypothetical prote	dynein beta heavy	probable 1-acylgly	related to BCS1 pr	hypothetical prote	densin-180 - rat	hypothetical prote	genome polyprotein	ALR protein - huma	ALR protein - huma	probable lpgR prot	malic acid transpo	malic acid transpo	hypothetical prote	hypothetical prote	hypothetical prote
C84480	T14914	D64688	T49717	A84089	T31434	T13250	MNWWHE	T03455	T03454	F70812	B64395	H64371	AH3166	AI2516	T39050
7	N	N	7	7	N	N	н	ĸ	N	~	N	N	N	N	7
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27.	27.5	27.	27.	27	27.	27.	27.	27.	27.	26.	26.	26.	56.	26.	56
	41	46.5	5.5	6.5	6.5	16.5	46.5	46.5	46.5	46	46	46	46	46	46
47	4	46	4	4	4	•									

ALIGNMENTS

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A;Accession: JC7607
A;Molecule type: DNA
A;Cross-references: DDBJ:AB040612; DDBJ:AB040613
C;Comment: This peptide induces arachidonic acid metabolite release from rat anterior p
release, and stimulation of ACTH secretion from the pitultary.
C;Genetics:
A;Gene: PRP
A;Introns: 33/1
prolactin-releasing peptide - rat
CiSpecies: Rattus norvegicus (Norway rat)
CiSpecies: Rattus norvegicus (Norway rat)
Cipate: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 30-Jun-2001
CiAccession: 407607
RiYamada, M.; Ozawa, A.; Ishii, S.; Shibusawa, N.; Hashida, T.; Ishizuka, T.; Hosoya, T.
RiYamada, M.; Ozawa, A.; Ishii, S.; Shibusawa, N.; Hashida, T.; Ishizuka, T.; Hosoya, T.
Airine: Isolation and characterization of the rat prolactin-releasing peptide gene: Mu A; Reference number: 407607; MUID:21092785; PMID:11178959
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83.9%; Pred. No. 8.7e-15;
tive 1; Mismatches 4; Indels
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Matches
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1 SRITHRHSMEIRIPDINPAWYASRGIRPVGRF 31

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RESULT 2

Conserved hypothetical protein PA2151 [imported] - Recudomonas aeruginosa (strain PAO1) C;Species: Pseudomonas aeruginosa C;Species: Pseudomonas aeruginosa C;Species: Pseudomonas aeruginosa C;Species: Pseudomonas aeruginosa C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000 C;Accession: F93376 R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; B signover, C.K.; Pham, X.Q.; Erwin, A.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim Jature 406, 359-364, 2000 A;Tille: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic path A;Tille: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic path A;Status: preliminary

A;Molecule_type: DNA A;Residues: 1-664 <STO> A;Cross-references: GB:AE004642; GB:AE004091; NID:g9948163; PIDN:AAG05539.1; GSPDB:GN00 A;Experimental source: strain PAO1 C;Genetics: A;Gene: PA2151

Query Match

33.0%; Score 56.5; DB 2; Length 664;

Gaps

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C'Accession: R69099

C'Accession: P69099

Signith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; Oiu, D.R.; Doucette-Stamm, L.A.; Mang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, I. ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N. A. Bacteriol. 179, 7135-7135, 1997

A; Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funcal A; Reference number: A69000; MUID:98037514; PMID:9371463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:AE000805; GB:AE000666; NID:g2621213; PIDN:AAB84680.1; PID:g26211. A;Experimental source: strain Delta H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ritimmelreich, R.; Hilbert, H.; Plagens, H.; Pirkl, E.; Li, B.C.; Herrmann, R. Nucleic Acids Res. 24, 4420-4449, 1996
A; Title: Complete sequence analysis of the genome of the bacterium Mycoplasma pneumonia A; Reference number: S73327; MUID:97105885; PMID:8948633
                                                       Cjaccession: D87559
RiNierman, W.C.; Felddlyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, i. B.; Laub, M.T.; DeBoy, R.T.; Dodson, K.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolcn, J.; Brmolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.P. Proc. Natl. Acad. Sci. U.S.A. 98, 4135-4141, 2001
A; Fitle: Complete Genome Sequence of Caulobacter crescentus.
A; Reference number: A87249; MUID:21173698; PMID:11259647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Residues: 1-1882 <HIM>
A;Cross-references: EMBL:AE000017; GB:U00089; NID:g1673812; PIDN:AAB95806.1; PID:g16738
A;Note: the nucleotide seguence was submitted to the EMBL Data Library, November 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bensory transduction histidine kinase - Methanobacterium thermoautotrophicum (strain D\epsilon
                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: DNA
A;Residues: 1-637 <STO>
A;Cross-references: GB:AE005673; NID:g13424056; PIDN:AAK24472.1; GSPDB:GN00148
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A, Status: preliminary; nucleic acid sequence not shown; translation not shown
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A,Status: preliminary; nucleic acid sequence not shown; translation not shown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CiSpecies: Mycoplasma pneumoniae
A;Variety: ATCC 29342
C;Date: 27-Feb-1997 #sequence_revision 25-Apr-1997 #text_change 07-Dec-1999
C;Accession: S73484; S62840
                        C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C.Species: Methanobacterium thermoautotrophicum
C.Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30.4%; Score 52; DB 2; Length 785; 46.4%; Pred. No. 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31.0%; Score 53; DB 2; Length 637, 48.0%; Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HRATFRIRRPDGNYRWVEYVDRPIRTDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            || | ::|:| |||| | :| | HRDSDDLRSPAINPAAIRVRILRAV 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 HRHSMRIRTPDINPAWYASRGIRPV 28
Species: Caulobacter crescentus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 46.4
nes 13; Conservative
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                                                                                                                                                                                                                                                                                                                                   A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Gene: CC2501
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Matches
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                                                                                                                                                                                                                                                                                                                            hyporhetical protein F15G16.60 - Arabidopsis thaliana C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Dates: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C; Accession: T47959
R; De Haan, M.; Maarse, A.C.; Grivell, L.A.; Mewes, H.W.; Lemcke, K.; Mayer, K.F.X.; Quet submitted to the Protein Sequence Database, January 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein Rv3485c - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Accession: B70569
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Comnor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Acterence number: A70500; MUID:98295987; PMID:9634230
A;Accession: B70569
A;Accession: preliminary; nucleic acid sequence not shown; translation not shown
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C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
F;46-227/Domain: short-chain alcohol dehydrogenase homology <SADH>
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                                      IndelB
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A,Experimental source: cultivar Columbia; BAC clone F15G16
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1. Similarity 27.5%; Pred. No. 4.2;
11; Conservative 5; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5.
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ilarity 52.6%; Pred. No. 9.7;
Conservative 3; Mismatches
   Pred. No. 3.5;
4; Mismatches
                                                                                                                                              4 HRHSMEIRTPDINPAWYASRGIRP 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Map position: 3
A;Introns: 39/1; 678/2; 698/3; 773/2
A;Note: F15G16.60
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Best Local Similarity 45.8%;
Matches 11; Conservative
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Best Local Similarity
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A; Residues: 1-790 <DEH>
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A;Status: preliminary
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Matches
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Gaps 7

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AH2016

AH2016

AH2016

Dispothetical protein allie86 [imported] - Nostoc sp. (strain PCC 7120)

C) Species: Nostoc sp. PCC 7120

A,Note: Nostoc sp. strain PCC 7120

A,Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120

C,Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002

C,Accession: AH2016

R,Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguch

R,Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguch

R,Kaneko, T.; Nakamura, S. Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, :

DNA Res. B, 205-213, 2001

A,Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium An.

A,Reference number: AB1807; MUID:21595285; PMID:11759840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: DNA
Ryesidues: 1-176 «JAD»
A;Cross-references: EMBL:275161; NID:g1420572; PID:e252411; PID:g1420573; GSPDB:GN00015
A;Experimental source: strain S288C
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A;Experimental source: strain 0157:H7, substrain RIMD 0509952
                                                                                                                                                                                                              Cispecies: Saccharomyces cerevisiae
Cispecies: Saccharomyces cerevisiae
Cipaces 12-101-1996 #sequence_revision 12-Jul-1996 #text_change 19-Apr-2002
Ciaccession: S67150
RiJauniaux, J.C.; Poirey, R.
submitted to the Protein Sequence Database, July 1996
A;Reference number: S67143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 176;
                                                                                                                                                     hypothetical protein YOR253w - yeast (Saccharomyces cerevisiae)
N/Alternate names: hypothetical protein 05315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 28.7%; Score 49; DB 2; Length 72; Best Local Similarity 34.5%; Pred. No. 3.9; Matches 10; Conservative 5; Mismatches 14; Indels
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           11 SPENNQSLDCSSPDPSRKWYQARLFSFGITPTG 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     120 SECHQHNVFVYLPAVDDLTKQWFIAHGFEQVG 151
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Pred. No. 8.7;
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28.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C,Genetics:
A,Gene: MIPS:YOR253w
A,Cross-references: SGD:S0005779
A,Map position: 15R
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Best Local Similarity 28.11
Best Local 9; Conservative
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A;Molecule type: DNA
A;Residues: 1-72 <HAY>
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A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-128 <KAN>
A;Cross-references: ENGL:D90917; GB:AB001339; NID:g1653836; PIDN:BAA18867.1; PID:d101966
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Species: Synechocystis sp.
A; Variety: PCC 6803
C; Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999
C; Accession: 876955
R; Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, B.; Nakamura, Y.; Miyajima, N.; O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda DNA Res. 3, 109-136, 1996
A; Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein 1 - Clostridium barkeri (fragment)
C;Species: Clostridium barkeri
C;Date: 19-Mar-1997 #sequence_revision 18-Jul-1997 #text_change 05-Nov-1999
C;Accession: $77900; $43551
C;Accession: $77900; $43551
B;Beatrix, B.; Zelder, O.; Linder, D.; Buckel, W.
Eur. J. Biochem. 221, 101-109, 1994
A;Title: Cloning; sequencing and expression of the gene encoding the coenzyme B(12)-dependence number: $43237; MUID:94222050; PMID:8168499
A;Accession: $77900
R;Hilbert, H.; Himmelreich, R.; Plagens, H.; Herrmann, R.
Nucleic Acids Res. 24, 628-639, 1996
A;Tilla: Sequence analysis of 56 kb from the genome of the bacterium Mycoplasma pneumoni A;Reference number: 862797; MUID:96177562; PMID:8604303
                                                                                                                                                     A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-1848 <HILD-A;Residues: 1-1848 <HILD-A;Cross-references: EMBL:U34816; NID:g1209514; PIDN:AAC43650.1; PID:g1209522 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1995
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Pred. No. 5.2;
6; Mismatches 12; Indels
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1. Similarity 42.9%; Pred. No. 5;
15; Conservative 2; Mismatches 12; Indela
                                                                                                                                                                                                                                                                                                                                                                                      Score 50.5; DB 2; Length 1 Pred. No. 82; 6; Mismatches 12; Indels
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A;Accession: $76955
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Best Local Similarity 33.3%;
Matches 11; Conservative (
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Best Local Similarity 32.3%;
Matches 10; Conservative
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A/Molecule type: DNA
A/Residues: 1-123 <BEA>
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Matches 15; Conserv
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probable glutathione S-transferase PA2821 [imported] - Pseudomonas aeruginosa (strain I C;Species: Pseudomonas aeruginosa (c;Species: Pseudomonas aeruginosa (c;Species: Pseudomonas aeruginosa (c;Species: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 23-Mar-2001 (c;Species: C;Species: C;
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A;Reaidues: 1-220 <STO>
A;Cross-references: GB:AE004709; GB:AE004091; NID:g9948904; PIDN:AAG06209.1; GSPDB:GNO(
A;Experimental source: strain PAO1
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5; Mismatches 12; Indels
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11; Conservative
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C;Species: Agrobacterium tumefaciens
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R;Bevan, M.; Van Der Schueren, J.; Chuang, Y.J.; Voet, M.; Robben, J.; Volckaert, G.; Submitted to the Protein Sequence Database, December 1999
A;Reference number: Z23009
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A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Accession: AC3169
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A;Cross-references: GB:AE008687; PIDN:AAL45769.1; PID:g17743503; GSPDB:GN00188
A;Experimental source: strain C58 (Dupont)
                                                A;Status: preliminary
A;Motacule type: DNA
A;Residues: 1-303 «KUR»
A;Cross-references: GB:BA000019; PIDN:BAB78052.1; PID:g17135506; GSPDB:GN00179
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: all1686
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 04-Feb_2000 #sequence_revision 04-Feb-2000 #text_change 04-Feb-2000
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A;Introns: 64/1; 739/3; 785/2; 1302/2; 1318/3; 1399/2; 1434/2
A;Note: F13G24.180
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A;Experimental source: cultivar Columbia; BAC clone F13G24
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              226 HEHSYE-RTRAIDGTTYLTCGAGAGNRPVGR 255
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A; Residues: 1-1501 <BEV>
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A;Molecule type: DNA
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     A; Accession: AH2016
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A;Gene: Atu5077
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1 SRTHRHSMEIRTPDINPAWYASRGIRPVGRF 31
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	Qwi oad	Cwiesbrot 41.*	*				ဗ င	Homo sapi
	10011	1.					8	Mammalia;
	o. is the	number	ų.	is the number of results predicted by cha	chance to have	8	88	NCBI_TaxI
and is	derived by	n or ed analy	qua 918	score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	suit being ribution.	princed,	3 2 2	SEOUENCE
	•	•					2	TISSUR-Br
	de			SUMMARIES			X &	MEDLINE=9
	Query						8	Kitada C.
. Score	Σ	ength 1	8	ID	Description	ion	a:	Kurokawa
17	1000	27	¦ -	Newton Godo	4 555 FAG	DELOCATION CONTROL	KT.	Nature 39
158		86	-	PRRP_BOVIN	P81264 b	bos taurus	2 22	[2]
3 149		83	-	PRRP RAT		rattus norv	RP	TISSUE SP
2	54 31.6	428	-	NER3 HUMAN		homo sapien	ž	MEDIINE=9
		288	-	Y587_PASMU		pasteurella	æ	Pujii R.,
50.5		1882	-	Y468 MYCPN		mycoplasma	RA	Sekiguchi
2 20		428	٦,	NER3 BOVIN		bos taurus	3 1	Sumino Y.
47.5	27.8	345	٦,	ARGC BACHD		bacillus ha	RT	Tissue d
47.5		200	٦.	CNC_DROME	P20482 0	drosopnila		receptor.
47		676	4 ~	EX.L HUMAN		bomo sapien	3 S	- I - FUNCT
2 46.5		240	-	PLSC HELPY		helicobacte	ខ	expre
3 46.5		1693	н	POLN HEVBU		hepatitis e	႘	lacto
46.5		1693	н	POLN_HEVMY		hepatitis e	႘	-I- TISSU
46.		1783	-	Y468_MYCGE		mycoplasma	႘	
4.		342	-	Y762 METUA		methanococc	႘	This SWIS
4.		347	٦,	Y576 METJA		methanococc	ខ្ល	between
	40 70.9	7 7	٠,	CYCK CHKVI		chromatium	ပ္ပ	cue surob
* 4	46 26.9	417	- ۲	EX /L CORGL	Canrais	corynebacte	38	modified
. 4	46 26.9	1400	-	RIF1_SCHPO		schizosacch	ខ	entities
45.		239	-	6 PGL_SYNY3		synechocyst	ខ	or send a
3 45.		407	-	Y116_MYCTU		mycobacteri	႘	
4		213	н.	SRN2 YEAST		Baccharomyc	S.	EMBL; ABO
4.		321	, i	HTPX_AGRIS		agrobacteri	ž i	MIM; 6026
4.		3.50	٠,	HMRO DROME		drosophila	ž i	30:00:00:00:00:00:00:00:00:00:00:00:00:0
* •		2 0	٠,	ices scout		escherichia	2 1	HOLIMOIDE;
7 3	2000	20 0	٦,	UNK KAT		rattus norv	. 6	SIGNAL
4.4		3 C	٠,	UVKA VIBCH		Vibrio cnol	Z	PEFILDE
* *		700	٠,	UVKA METTH		methanobact	Z [PEFTIDE
1 4 4 V T		973 673	٦.	UVRA RHILO		rhizobium 1	1 6	MOPEP MODE
4 40	26.3	7 0		UVKA KHIME	P56899 T	rnizobium m	1 0	ACU KES
ŗ		000	4	VGIZ_BFBU3		bacteriopna	ה מ	SPCODINCE

Q995n0 schizosacch P18897 rattus norv P775c2 secherichia P54974 agrobacteri P30143 secherichia P31795 radiation m P17812 homo saplen P32770 saccharomyc P03357 akr murine Q9uia9 homo saplen Q9epk7 mus musculu P03356 akv murine
YH85 SCHPO SMR2_RAT YAJW ECOLI CRTY_AGRAU YAAJ ECOLI POL MLVRK PYRG HUWAN NRP1 YEAST POL WLVAK XPO7_HUWAN XPO7_HUWAN
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## ALIGNMENTS

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lept. 83:1-10(1999).
TION: Stimulates prolactin (PRL) release and regulates the
Ession of prolactin through its receptor GPRIO. May stimulate
otrophs directly to secrete PRL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    98266781; PubMed=9607765;

., Habata Y., Fujii R., Kawamata Y., Hosoya M., Fukusumi S.,

., Masuo Y., Asano T., Marsumoto H., Sekiguchi M.,

(T., Nishimura O., Onda H., Fujino M.;

ctin-releasing peptide in the brain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9942652; PubMed=10498338;
, Fukusumi S., Hosoya M., Kawamata Y., Habata Y., Hinuma S.,
ii M., Kitada C., Kurokawa T., Nishimura O., Onda H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ., Fujino M.;
distribution of prolactin-releasing peptide (PrRP) and its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AMIDATION (G-54 PROVIDE AMIDE GROUP).
229A2F3F50CF981B CRC64;
                                                                                                                      000 (Rel. 39, Last sequence update)
003 (Rel. 41, Last annotation update)
.n-releasing peptide precursor (PrRP) (Prolactin-releasing
[Contains: Prolactin-releasing peptide PrRP31; Prolactin-
                                                                                                                                                                                                                                                                                                   a, Metazoa; Chordata, Craniata, Vertebrata; Buteleostomi; Butheria; Primates; Catarrhini; Hominidae; Homo.
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PROLACTIN-RELEASING PEPTIDE PRRP20.
                                               87 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          563; -.
305180; F:peptide hormone; TAS.
                                                 PRT;
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                                                                                                   (Rel. 39, Created)
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9639 MW;
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                                                                                                                                                                                                                            g peptide PrRP20].
                                                 STANDARD;
                                                                                                                                                                                                                                                                              iens (Human)
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34
58
53
87 AA;
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                                               TOMAN
RESULT 1
PRRP HUMAN
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Prolactin-releasing peptide precursor (PrRP) (Prolactin-releasing hormone) [Contains: Prolactin-releasing peptide PrRP31; Prolactin-
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                                                                                                                                                 NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          receptor."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hinuma S., Habata Y., Fujii R., Kawamata Y., Hosoya M., Fukusumi S., Kitada C., Masuo Y., Asano T., Matsumoto H., Sekiguchi M., Kutada C., Masuo Y., Asano T., Matsumoto H., Sekiguchi M., Nushimura O., Onda H., Fujino M.; A prolactin-releasing peptide in the brain."; Nature 393:272-276(1998).

-I. FUNCTION: Stimulates prolactin (PRL) release and regulates the expression of prolactin through its receptor GPR10. May stimulate lactotrophs directly to secrete PRL.

-I TISSUE SPECIFICITY: MEDULLA OBLONGATA AND HYPOTHALAMUS.
                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                          30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Prolactin-releasing peptide precursor (PrRP) (Prolactin-releasing hormone) (Contains: Prolactin-releasing peptide PrRP31; Prolactin-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AMIDATION (G-54 PROVIDE AMIDE GROUP)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROLACTIN-RELEASING PEPTIDE PRRP20
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Hormone; Amidation; Signal; Cleavage on pair of basic residues.
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                        100.0%; Score 171; DB 1; Length 87; 100.0%; Pred. No. 4.8e-19;
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                                                                  IndelB
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1; Mismatches 2;
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                                                                                                                                                                                                                                                       98 AA.
                                                                                                         1 SRTHRHSMEIRTPDINPAWYASRGIRPVGRF 31
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                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., AND SEQUENCE OF 23-52
                                                                                                                                23 SRIHRHSMEIRIPDINPAWYASRGIRPVGRF
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                                                                                                                                                                                                                                                    PRT;
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                                                                31; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                taurus (Bovine).
                                            Similarity
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PRRP_RAT
ID PRRP_RAT
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                        Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEGUENCE FROM N.A. (ISOFORM 2).
STRAIN-Sprague-Dawley; TISSUE-Hypothalamus;
Anderson S.T., Kokay I.C., Lang T., Grattan D.R., Curlewis J.D.;
"Quantitation of prolactin-releasing peptide (PrRP) mRNA expression in specific brain regions during the rat oestrous cycle and in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TPDINPAMYTGRGIRPVGRFGRRRATPRDVTGLGQLSCLPL
DGRTKPSQRG -> SECLTYGRQPLTSPHPFTSQMPP (in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -1- FUNCTION: Stimulates prolactin (PRL) release and regulates the expression of prolactin through its receptor GPR10. May stimulate lactotrophs directly to secrete PRL.
                                                               Rattus norvegicus (Rat).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                      Hinuma S., Habata Y., Fujii R., Kawamata Y., Hosoya M., Fukusumi S., Kitada C., Masuo Y., Asano T., Mateumoto H., Sekiguchi M., Kurokawa T., Nishimura O., Onda H., Fujino M.; M. Maroin-releasing peptide in the brain.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sumino Y., Pujino M.; Trismer and its "Tissue distribution of prolactin-releasing peptide (PrRP) and its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AMIDATION (G-53 PROVIDE AMIDE GROUP).
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-!- TISSUR SPECIFICITY: Widely expressed, with highest levels in medulla oblongata and hypothalamus.
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PROLACTIN-RELEASING PEPTIDE PRRP20.
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Pujii R., Fukusumi S., Hosoya M., Kawamata Y., Habata Y., Hi
Sekiguchi M., Kitada C., Kurokawa T., Nishimura O., Onda H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 149; DB 1; Length 83;
Pred. No. 9.8e-16;
1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    lactation.";
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               isoform 2).
/FTId=VSP 004370.
DOC75A264EEB4F29 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     lsoId=P81278-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                     MEDLINE=98268781; PubMed=9607765;
                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AB015418; BAA29026.1; -.
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Local Similarity 83.9%;
es 26; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Regul. Pept. 83:1-10(1999).
releasing peptide PrRP20]
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PIR; JC7607; JC7607.
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Bimilarity

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                                                                                                                                                                                                                                                                           NER3 HUMAN STANDARD; PRT; 428 AA.
Q9UQ49; Q9NOB1;
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Sialidase 3 (RC 3.2.1.18) (Membrane stalidase) (Ganglioside stalidase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
TISSUB-Brain,
MEDLINE=9933535
MARGIAL T., WORNING S., Kuwabara M., Akita H., Miyagi T.;
"Cloning, expression, and chromosomal mapping of a human ganglioside"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Monti E., Bassi M.T., Papini N., Riboni M., Manzoni M., Venerando B., Croci G., Preti A., Ballabio A., Tettamanti G., Borsani G.; "Identification and expression of NRU3, a novel human sialidase associated to the plasma membrane."; Blochem. J. 349:1343-351(2000).
-!- FUNCTION: Plays a role in modulating the ganglioside content of the lipid bilayer at the level of membrane-bound sialyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 glycoconjugates.
--- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->8) -, alpha-(2->6) -, alpha-(2->8)-glycosidic linkages of terminal stalic residues in oligosaccharides, glycoproteins, glycolipids, colominic acid and synthetic substrates.
--- SUBCELLULAR LOCATION: Membrane-associated.
--- TISSUE SPECIFICITY: Highly expressed in skeletal muscle, testis, adrenal gland and thymus, followed by pancreas, liver, heart and thymus weakly expressed in kidney, placenta, brain and lung.
--- MISCELLANBOUS: Optimum pH is 3.8.
--- SIMILARITY: BELONGS TO FAMILY 33 OF GLYCOSYL HYDROLASES.
--- SIMILARITY: Contains 3 BNR repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; Y18563; CAB96131.1; ALT_INIT.
Genew; HGNC; 7760; NEU3.
MIM; 60617; --
GO; GO:0005887; C:integral to plasma membrane;
GO; GO:0006689; P:ganglioside catabolism; TAS.
InterPro; PRO2012; BNR; 3.
Hydrolase; Glycosidase; Membrane; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Biochem. Biophys. Res. Commun. 261:21-27(1999)
                                 31
                                                                   22 SRAHQHSMETRTPDINPAWYTGRGIRPVGRF 52
                              SRTHRHSMEIRTPDINPAWYASRGIRPVGRF
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BNR 3.
FRIP MOTIF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (N-acetyl-alpha-neuraminidase 3).
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TISSUE=Skeletal muscle;
PubMed=10861246;
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REPEAT
SITE
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ID NER3 HUMAN

ID NER3 HUMAN

ID 28-FEB-

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                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria, Proteobacteria, Gammaproteobacteria, Pasteurellales,
Pasteurellaceae, Pasteurella.
NCBI_TaxID=747;
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InterPro; IPR005581; Fructosamin kin.
Pfam; PF03881; Fructosamin kin; I.
Hypothetical protein; Transferae; Kinase; Complete proteome.
SEQUENCE 288 AA; 33778 MW; P4D2F6C26014D940 CRC64;
                                                                                                                                                                                                        Score 54; DB 1; Length 428;
Pred. No. 1.5;
6; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30.4%; Score 52; DB 1; Length 288; 37.5%; Pred. No. 2;
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                                                                                                                                                   Potential.
35D1DD9359A78C98 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                 16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical protein PM0587.
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ID Y468 MYCPN STANDARD; PRT; 1882 AA.

AC P75109; Q50317;

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 128-FEB-2003 (Rel. 41, Last annotation update)

B Protein MG468 homolog (K05_orf1882).
                                   Potential.
Potential.
Potential.
Potential.
By similarity.
Potential.
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                                                                                                                                                                                                                                                                                                          2 RTHRHSMBIRTPDINPAWYASRGIRPV 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 RHSMEIRTPDINPAWYASRGIRPV 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=21145866; PubMed=11248100;
                                                                                                                                                                         48252 MW;
                                                                                                                                                                                                            31.6%;
                                                                                                                                                                                                                              37.0%;
                                                                                                                                                                                                                            l Similarity 37.0
10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
 25
45
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225
245
340
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9; Conservat
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346
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428
428
445
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ACT SITE
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Y587_PASMU
                                                                                                                                                                                                                                            Matches
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28-FEB-2003 (Rel. 41, Last annotation update)
Sialidase 3 (BC 3.2.1.18) (Membrane sialidase) (Ganglioside sialidase)
(N-acetyl-alpha-neuraminidase 3).
                                                                                                                                                                                                                                                                                                                                                                         glycoconjugates.
--- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-, alpha-(2->8)-glycosidic linkages of terminal sialic residues in oligosaccharides, glycoproteins, glycolipids, colominic acid and synthetic substrates.
--- SUBCELLULAR LOCATION: Membrane-associated (By similarity).
--- TISSUE SPECIFICITY: Expressed in brain.
--- SIMILARITY: BELONGS TO FAMILY 33 OF GLYCOSYL HYDROLASES.
                                                                                                                                                                                                                        MEDLINE-99143165; PubMed-9988745;
Miyagi T., Wada T., Iwamatsu A., Hata K., Yoshikawa Y., Tokuyama S.,
Sawada M.;
                                                                                                                                                                                                                                                                         "Molecular cloning and characterization of a plasma membrane-associated stalidase specific for gangliosides.";
J. BAO1. Chem. 274:5004-5011 (1999).
-I. FUNCTION: Plays a role in modulating the ganglioside content of the lipid bilayer at the level of membrane-bound stalyl
                                                                    Bos taurus (Bovine).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                       SEQUENCE FROM N.A., PARTIAL SEQUENCE, AND CHARACTERIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 428;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BNR 1.
BNR 2.
BNR 3.
RIP MOTIF.
By similarity.
Potential.
Potential.
Potential.
Potential.
Potential.
By similarity.
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Pred. No. 6
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InterPro; IPR0202860; GH_BNR.
Pfam; PF02012; BNR; 3.
Hydrolase; Glycosidase; Membran
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Rel. 41, Created)
(Rel. 41, Last sequ
(Rel. 41, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           47916 MW;
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428 AA;
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Best Local Similarity
                                                                                                                                                NCBI_TaxID=9913;
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28-FEB-2003
28-FEB-2003
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ACT SITE
SEQUENCE
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ARGC_BACHD
ID ARGC_BAC
AC Q9K8V2;
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SITE
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                                                                                                                                                                                                                                                                                                                Hilbert H., Himmelreich R., Plagens H., Herrmann R.; "Sequence analysis of 56 kb from the genome of the bacterium Mycoplasma pneumoniae comprising the dnaA region, the atp operon and a cluster of ribosomal protein genes."; Nucleic Acids Res. 24:628-639(1996).
                                                                                                                                                                                       'Complete sequence analysis of the genome of the bacterium Mycoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Towards a two-dimensional proteome map of Mycoplasma pneumoniae.";
Electrophoresis 21:3765-3780(2000).
-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-!- SIMILARITY: SOME, TO MG064.
                   Mycoplasma pneumoniae.
Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
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                                                                                                                                                                                                                                                                                                                                                                                                                               IDENTIFICATION BY MASS SPECTROMETRY.
STRAIN=ATCC 29342 / M129;
MEDLINE=21088919; PubMed=11271496;
MEGLIA J.T. Ubebra B., Boguth G., Goerg A., Schnoelzer M., Herrmann R., Frank R.;
                                                                                                                                                Himmelreich R., Hilbert H., Plagens H., Pirkl B., Li B.-C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               209442 MW; 03CFA4D99A7120ED CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 SRTHRHSMEIRTPDINPAWYASRGIRPVGRF 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Rel. 41, Created)
(Rel. 41, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 50.5;
Pred. No. 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL. POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL
                                                                                                                                                                                                           pneumoniae.";
Nucleic Acids Res. 24:4420-4449(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                           SEQUENCE OF 1-1848 FROM N.A.
STRAIN=ATCC 29342 / M129;
MEDLINE=96177562; PubMed=8604303;
                                                                                                             STRAIN=ATCC 29342 / M129;
MEDLINE=97105885; PubMed=8948633;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AE000017; AAB95806.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 U34816; AAC43650.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; S73484; S73484.
InterPro; IPR003838; DUF214.
Pfam; PF02687; Ft8X; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10; Conservative
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                                                                                           SEQUENCE FROM N.A.
                                                        NCBI_TaxID=2104;
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1828
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1882
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ID NER3 BOVIN

AC 097859;

DT 28-FEB-2003 (

DT 28-FEB-2003 (
                                                                                                                                                                  Herrmann R.;
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Similarity 37.5
9; Conservative
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529
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387
497
349
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Q9FBM3;
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60; 60:00
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60; 60:00
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셤
                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMED outstainnthe European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this etatement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1;
                                                                                                                                SEQUENCE FROM N.A.
MEDLINE=92001535; PubMed=1911393;
Mohler J., Vani K., Leung S., Epstein A.;
"Segmentally restricted, cephalic expression of a leucine zipper gene during Drosophila embryogenesis.";
Mech. Dev. 34:3-9(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
N-acetyl-gamma-glutamyl-phosphate reductase (EC 1.2.1.38) (AGPR) (N-
          -glutamate semialdehyde dehydrogenase) (NAGSA dehydrogenase).
                                                                                                     Sasaki R., Masui N.
                                                                                                                                                                                                                                                                                                      EMBL; AP001517; BAB06619.1; -.
PIR; D84012; D84012.
HAMAP; MP 00150; -; 1.
InterPro; IRR000706; AGPR act site.
InterPro; IRR000534; Semialdh-dh.
Pfam; PF02174; Semialdhyde-dh; 1.
ProDom; PF02774; Semialdhyde-dhc; 1.
ProDom; PF02174; ARGC; 1.
PROSITE; P$01224; ARGC; 1.
Arginine blosynthesis; Oxidoreductase; NADP; Complete proteome.
ACT SITE 149 149 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa, Arthropoda; Héxapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 345;
                                                                                STRAIN=C-125 / JCM 9153;
BEDLINE=20512582; PubMed=11058132;
Takami H., Nakagone K., Takaki Y., Maeno G., Sasaki R., M
Fuji P., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9; Indels
                                    Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus
NCBI_TaxID=86665,
                                                                                                                                                                                                                                                                                                                                                                                                                               345 AA; 38188 MW; 3R9F45DD09FC68EA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Rel. 17, Created)
(Rel. 33, Last sequence update)
(Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 12;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                  27.8%; Score 47.5; 45.5%; Pred. No. 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster (Fruit fly)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                101 LRINEPDVYEAWY-KROAAPVG 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8 MEIRTPDINPAWYASRGIRPVG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Segmentation protein cap'n'collar.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             45.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                             Bacillus halodurans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                            [1] -
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-FEB-1991
01-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CNC_DROME
P20482;
                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DROME
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GO; GO:0005634; C:nucleus; IDA.
GO; GO:0005634; C:nucleus; IDA.
GO; GO:000350; P:Dlascoderm segmentation; IMP.
GO; GO:0007310; P:Ocoyte dorsal/ventral axis determination; IMP.
GO; GO:00042070; P:Ocoyte nucleus anchoring; IMP.
GO; GO:0008103; P:polarization of the ocoyte microtubule cyto. .; IMP.
GO; GO:0008139; P:regulation of pole plasm bicoid mRNA locali. .; IMP.
GO; GO:0007317; P:regulation of pole plasm oskar mRNA localiz. .; IMP.
InterPro; IPR00422; TF_DIP.
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FUNCTION: PLAYS A ROLE IN CEPHALIC PATTERNING. PROBABLE SUBUNIT
OF A HETERODIMERIC REGULATORY PROTEIN INVOLVED IN THE CONTROL OF
                                                                                                          DEVELOPMENTAL STAGE: LOCALIZED TO THE MANDIBULAR SEGMENT AND THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L., Thomson N.R., James K.D., Harris D.E., Quall M.A., Kieser H., Harper D., Bateman A., Bolow S., Chandra G., Chen C.W., Collins M., Cronin A., Fraser A., Golbe A., Hidalgo J., Hornsby T., Howarth S., Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS50217; BZIP; 1.
PROSITE; PS00036; BZIP BASIC; 1.
Transcription regulation; Activator; DNA-binding; Nuclear protein;
                                                                                                                                            HYPOPHARYNGEAL AND LABRAL PRIMORDIA FIRST DETECTABLE IN LATE BLASTODERM STAGES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1;
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28-FEB-2003 (Rel. 41, Last annotation update)
Probable exodeoxyribonuclease VII large subunit (RC 3.1.11.6)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptomyces coelicolor.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 533;
                                                                                                                                                                                                                SIMILARITY: Belongs to the bZIP family. CNC subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             349 I -> L (IN REF. 1; AAB59246)
56948 MW; RADFP9ASD6CASCSF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptomycineae; Streptomycetaceae; Streptomyces,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LEUCINE-ZIPPER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 47.5; DE Fred. No. 19; 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         402 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GLN-RICH.
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MEDLINE=21996410; PubMed=12000953;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Exonuclease VII large subunit).
XSEA OR SCO5056 OR SCK7.29C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-OCT-2001 (Rel. 40, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M37495; AAB59246.1; -. HSSP; P34707; ISKN. HSMSPA. T01998; -. FlyBase; FBgn0000338; cnc.
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Transmembrane;
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TRANSMEM
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PLSC_HELPY
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EMBL;
EMBL;
EMBL;
EMBL;
EMBL;
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                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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MEDLINE=97189339; PubMed=9037597;
Wise C.A., Clines G.A., Massa H., Trask B.J., Lovett M.;
"Identification and localization of the gene for EXTL, a third member of the multiple exostoses gene family.";
Genome Res. 7:10-16(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A., AND VARIANT HIS-379.
MEDLINE=99408231; PubMed=10480354;
Xu L., Xia J., Jiang H., Zhou J., Li H., Wang D., Pan Q., Long Z.,
Fan C., Deng H.-X.;
"Mutation analysis of hereditary multiple exostoses in the Chinese.";
Hum. Genet. 105:45-50(1999).
                                      Hopwood D.A.;
"Complete genome sequence of the model actinomycete Streptomyces
"Complete genome sequence of the model actinomycete Streptomyces
coelicolor A3(2).";
Nature 417:141-147(2002).
--- FUNCTION: BIDIRECTIONALLY DEGRADES SINGLE-STRANDED DNA INTO LARGE
ACID-INSOLUBLE OLIGONUCLEOTIDES (BY SIMILARITY).
INTO SMALL ACID-SOLUBLE OLIGONUCLEOTIDES (BY SIMILARITY).
--- CAPALYTIC ACITIVITY: Exonucleolytic cleavage in either 5'- to 3'-
or 3'- to 5'-direction to yield nucleoside 5'-phosphates.
--- SUBUNIT: Heterooligomer composed of large and small subunits (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-SEP-2003 (Rel. 36, Last sequence update)
Exostosin-like 1 (EC 2.4.1.224) (Glucuronosyl-N-acetylglucosaminyl-protecoglycan 4-alpha-N-acetylglucosaminyltransferase) (Exostosin-L)
EXTL OR EXTL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      th 27.5%; Score 47; DB 1; Length 402; Similarity 47.6%; Pred. No. 16; 10; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                             EMBL; AL939122; CAC05901.1; -.
HAMAP; MF 00378; -; 1.
InterPro; IPR003753; EXNuc VII L.
InterPro; IPR004365; IRNA anti.
Pfam; PF0136; IRNA anti.
Pfam; PF0136; IRNA anti.
IGRAMs; TIGR0037; ASSA; 1.
Hydrolase; Nuclease; Exonuclease; Complete proteome.
SEQUENCE 402 AA; 43882 MW; 145929A8372B4E08 CRC64;
                                                                                                                                                                              similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: BELONGS TO THE XSEA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               676 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | ||| ||
| PEWYAPRGQLSLRAAEIKPVG 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PAWYASRG-----IRPVG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EXL1 HUMAN Q92935;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
**REQUENCE FROM N.A.*

**RUTHER P. 4.*

**WUTE W., Spieker N., Van Roy N., De Raepe A., De Boulle K.,

**WUTEME P. 4.*

**WUTEME P. 4.*

**WUTEME P. 4.*

**WUTEME P. 4.*

**Sedimed physical mapping and genomic structure of the EXTL1 gene.";

**Sedimed physical mapping and genomic structure of the EXTL1 gene.";

**Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: Probable glycosyltrandsrase (By similarity).

-!- CATALYTIC ACTIVITY: UDP-N acetyl.D-Glucosaminyl-proteoglycan =

UDP + N-acetyl-alpha-D-glucosaminyl-(1->4)-beta-D-glucuronosyl-

(1->4)-N-acetyl-alpha-D-glucosaminyl-proteoglycan.

(1->4)-N-acetyl-alpha-D-glucosaminyl-proteoglycan.

-!- SUBCELLULAR LOCATION: Type II membrane protein. Endoplasmic

reticulum: (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PLSC HELPY STANDARD; PRT; 240 AA.
025903;
15-DEC-1998 (Rel. 37, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
1-acyl-sn-glycerol-3-phosphate acyltransferase (EC 2.3.1.51) (1-AGP acyltransferase) (1-AGPAT) (Lysophosphatidic acid acyltransferase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LUMENAL (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                               -1- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27.5%; Score 47; DB 1; Length 676;
45.0%; Pred. No. 29;
tive 3; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Signal-anchor; Glycoprotein; Polymorphism 9 CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transferase; Glycosyltransferase; Endoplasmic reticulum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /FTId=VAR 012830.
676 AA; 74673 MW; B5E006AB762E5633 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genew; HGNC:3515; EXTL1.
MIM; 601738; -
GO; GO:0008181; F:tumor suppressor; TAS.
GO; GO:0001501; P:skeletal development; TAS.
InterPro; IPR004263; Exostosin.
Pfam; PF03016; Exostosin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      H -- N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF153980; AAF73172.1; -. EMBL; AF151391; AAF73172.1; JOINED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12 TPDINPAWYASRGIRPVGRF 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9; Conservative
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269
379
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Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AF083630;
AF083631;
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                                                                                                                                                                                                                                                -1- MISCELLANEOUS: HEPATITIS E VIRUS IS THE MAJOR CAUSATIVE AGENT OF
                                                                                                                                                                                            -1- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate
                                                                                                        "Hepatitis E virus (HEV): molecular cloning and sequencing of the full-length viral genome.";
Virology 185:120-131(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Polyprotein, Transferase, RNA-directed RNA polymerase, Helicase, ATP-binding.
              MEDLINE-92024067; PubMed=1926770;
Tam A.W., Smith M.M., Guerra M.E., Huang C.-C., Bradley D.W.,
Fry K.E., Reyes G.R.;
                                                                                                                                                                                                                                                                                ENTERICALLY TRANSMITTED NON-A, NON-B HEPATITIS (ET-NANBH)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR002589; Alpp.
InterPro; IPR001788; RNA_dep_RNApol2.
InterPro; IPR007095; RNA_pol_DS_PS.
InterPro; IPR007094; RNA_pol_PSVIr.
InterPro; IPR002588; V_methyltransf.
InterPro; IPR000606; Viral_helicasel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF01661; Alpp; 1.
Pfam; PF00978; RNA dep RNApol2; 1.
Pfam; PF01643; Viral helicase1; 1.
Pfam; PF01660; Vmethyltransf; 1.
SWART; SM00506; Alpp; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M73218; AAA45734.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEROPS; C41.001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POLN HEVMY
Q04610;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 14
POLN_HEVMY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matchea
ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ï
                                                                                                                                                                                MEDLINE-9739467; PubMed-9252185; MEDLINE-9739467; PubMed-9252185; MEDLINE-9739467; PubMed-9252185; MEDLINE-9739467; PubMed-9252185; Medline R.A., Sutton G.G., Frieschmann R.D., Ketchum K.A., Klenk H.-F., Gill S., Dougherty B.A., Nelson K., Quackenbush J., Zhou L., Kirkness B.F., Feterson S., Loftus B., Richardson D., Dodgon R., Khalak H.G., Glodek A., McKenney K., PitzGerald L.M., Lee N., Adams M.D., Hickey B.K., Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M., Cotton M.D., Weidman J.M., Fujii C., Bowman C., Watthey L., Wallin B., Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: CONVERTS LYSOPHOSPHATIDIC ACID (LPA) INTO PHOSPHATIDIC ACID BY INCORPORATING ACYL MOIETY AT THE 2 POSITION.
CATALYTIC ACTIVITY: Acyl-CoA + 1-acyl-sn-glycerol 3-phosphate = CoA + 1,2-diacyl-sn-glycerol 3-phosphate.
           Helicobacter pylori (Campylobacter pylori).
Bacteria; Proteobacteria; Epalionproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complete genome sequence of the gastric pathogen Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Non-structural polyprotein [Contains: RNA-directed RNA polymerase (BC 2.7.7.48); Helicase].
Hepatitis E virus (strain Burma) (HEV).
Viruses; seRNA positive-strand viruses, no DNA stage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PATHWAY: De novo phospholipid biosynthesis; second step. SUBCELLULAR LOCATION: Inner membrane-associated (Potential). SIMILARITY: BELONGS TO THE 1-ACYL-SN-GLYCEROL-3-PHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 240;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR002123; Acyltransferase.
InterPro; IPR004552; AGP acyltrn.
Pfam; PR01553; Acyltransferase; 1.
SMART; SM00563; PlsC; 1.
TIGRPAMs; ITGR00530; AGP acyltrn; 1.
Phospholipid biosynthesis; Transferase; Acyltransferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Inner membrane, Complete proteome.
SEGUENCE 240 AA; 27745 MW; 22BD5D0EB190BBDD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 46.5; DB 1;
Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT; 1693 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 47.6%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               197 ARTRLVMLESYTPDFNSPTWY 217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AE000636; AAD08393.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACYLTRANSFERASE FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hepatitis B-like viruses.
NCBI_TaxID=31767;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pylori.";
Nature 388:539-547(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     D64688; D64688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                           [1]
SEQUENCE FROM N.A.
                                                                                                                   NCBI_TaxID=210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TIGR; HP1348;
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1D POLM H

AC P29324

DT 01-DEC

DT 28-FBB

DB NOT-BE:

DB (RC 2:

OC Viruse

OC Viruse

OC Hepatil

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SOW DEATH AND DE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Virus Genes 7:95-109(1993).
-1- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence and gene structure of the hepatitis B virus isolated from
                                                                                                                                                                                                                                                                                    01-0cr.1993 (Rel. 27, Created)
01-0cr.1993 (Rel. 27, Last sequence update)
01-0cr.1993 (Rel. 41, Last sequence update)
01-0cr.2003 (Rel. 41, Last annotation update)
Non-structural polyprotein [Contains: RNA-directed RNA polymerase (RC 2.7.7.48); Helicasel.
Hepatitis B virus (strain Myanmar) (HEV).
Viruses; seRNA positive-strand viruses, no DNA stage;
Hepatitis B-like viruses.
NCBL_TaxID=31769;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE-9322757; PubMed-8470371;
Aye T.N. - Uchida T., Ma M.Z., Iida F., Shikata T., Ichikawa M.,
Rikihisa T., Winn K.;
                                                                                              1;
                                                         DB 1; Length 1693;
                                                                                              11; Indels
975 982 ATP (POTENTIAL).
1693 AA; 185191 MW; 2P355E46E9ED219B CRC64;
                                                                                                                                                                                                                                                                     PRT; 1693 AA.
                                                       27.2%; Score 46.5; D
37.0%; Pred. No. 96;
tive 5; Mismatches
                                                                                                                                                                        904 KNHRPGDELYLPELAARWFEANRPTRP 930
                                                                                                                                  2 RTHRHSMEIRTPDINPAWY-ASRGIRP 27
                                                                           Local Similarity 37.0
nes 10; Conservative
                                                                                                                                                                                                                                                       STANDARD;
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SOLUTION TO THE STANTANT OF THE SOLUTION OF TH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=ATCC 33530 / G-37;
MEDLINE=96026346; PubMed=7569993;
MEDLINE=96026346; PubMed=7569993;
MEDLINE=96026346; PubMed=7569993;
Praser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A.,
Prictohman R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M.,
Pritchman J.L., Weidman J.F., Small K.V., Sandusky W., Fuhrmann J.L.,
Pritchman J.T., Utterback T.R., Saudek D.M., Phillips C.A., Merrick J.M.,
Tomb J.-F., Dougherty B.A., Bott K.F., Hu P.-C., Lucier T.S.,
Peterson S. N., Smith H.O., Hutchison C.A. III, Veneer J.C.;
"The minimal gene complement of Mycoplasma genitalium.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A., Fleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M., Fritchman J.L., Weidman J.F., Small K.V., Sandusky M., Fuhrmann J.L., Nguyen D.T., Utterback T.R., Saudek D.M., Phillips C.A., Merrick J.M. Tomb J.-P., Dougherty B.A., Bott K.F., Hu P.-C., Lucier T.S., Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.; Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Polyprotein; Transferase; RNA-directed RNA polymerase; Helicase;
ATP-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma. NCBI TaxID=2097;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 1693;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    82 ATP (POTENTIAL).
185215 MW; AAB4C9140A7E21EA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1997 (Rel. 35, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical protein MG468.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT; 1783 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            . Match
Local Similarity 37.0%; Pred. No. 96;
les 10; Conservative 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        904 KNHRPGDELYLPELAARWFEANRPTRP 930
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                                                                                                                                                                                                                                                                                                                                               InterPro; IPR002589; Alpp.
InterPro; IPR001788; RNA_dep_RNApol2.
InterPro; IPR007094; RNA_pol_Ds_Ps.
InterPro; IPR007094; RNA_pol_Psyir.
InterPro; IPR007088; V_methyltransf.
InterPro; IPR000606; Viral_helicasel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF01661; Alpp; 1.
Pfam; PF00978; RNA dep RNApol2; 1.
Pfam; PF01443; Viral helicaeel; 1.
Pfam; PF01660; Vmethyltransf; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 879-985 FROM N.A.
STRAIN-ATCC 33530 / G-37;
MEDLINE-94075230; PubMed-8253680;
                                                                                                                                                                                                                                                                                       EMBL; D10330; BAA01172.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    975 98
1693 AA;
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Y468 MYCGE
AC 049460;
DT 01-NOV-1997
DT 15-JUL-1999
DT 16-OCT-2001
DE Hypothetical
GN MG468.
OS MYCOPLaema 9
OC Bacteria; Fi
OX NCBI_TAXID=2
RN SEQUENCE FRO
RC STRAIN-ATCC
RX MEDLINE=9602
RA PRASE C.M.,
RA PICHAMAN J.F.,
RA TOMD J.-F.,
RA PICHAMAN S.N
RT SCIENCE 270:
RN [2]
RN [2]
RN STAILCHAMAN J.
RA PICHAMAN J.
RA POMD J.-F.,
RA PULLAMAN J.
RA SUDMILLE GO
RN [3]
RN SUDMILLE GO
RN [3]
RN SUDMILLE GO
RN [3]
RN SEQUENCE OF
RC STRAINE-ATCC
RN MEDLINE-ATCC
RN MEDLINE-ATCC
RN MEDLINE-ATCC
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                     -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27.2%; Score 46.5; DB 1; Length 1783; 29.0%; Pred. No. 1e+02; ive 6; Mismatches 13; Indels 3.
Peterson S.N., Hu P.-C., Bott K.P., Hutchison C.A. III; A survey of the Mycoplasma genitalium genome by using random
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA; 200168 MW; 87BD575AEC2E374B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                            TIGR; MG468; -.
Interpro; IRR003838; DUP214.
PÉmi; PR05687; PteX; 1.
Hypothetical protein; Transmembrane; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1e+02;
13;
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                                               sequencing.";
J. Bacteriol. 175:7918-7930(1993)
                                                                                                                                                                                                                                                                                                                                        EMBL; U39728; AAC72488.1; -. EMBL; U01808; AAD12339.1; -. TIGR; MG468; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 29.0 Matches 9; Conservative
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1750
1772
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TRANSMEM
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OM protein

Run on:

Sequence:

Searched:

Database

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99eyb3 escherichia
099700 thermoplasm
095642 erigmatella
08fr15 xanthomonas
08fr37 uncultured
08fm14 corynebacte
08fm14 corynebacte
08fm14 corynebacte
08fm2 agreedentella
08ger0 xanthomonas
08102 bordetella
045375 bordetella
045375 bordetella
045375 bordetella
088002 bordetella
0894x2 bifidobacte
033440 mycobacteri
                                                                                                                                                                                                                                                                                                                                                     Q9vrv3 drosophila
Q9vp62 drosophila
Q9vy4 caenorhabdi
Q8lmf7 oryza sativ
Q8gsk7 oryza sativ
Q8gsk7 oryza sativ
P74747 synechocyst
Q91815 thodospiril
Q9280 hemicentrot
Q8rtv7 uncultured
Q8rtv7 uncultured
Q8fm04 corynebacte
Q06m04 corynebacte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
Cutlewis J.D., Kusters D.H.L., Barclay J.L., Anderson S.T.;
"Prolactin-releasing peptide (PrRP) in the ewe: CDNA cloning, mRNA distribution and effects on prolactin secretion in vitro and in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Preproprolactin-releasing peptide.
Ovis aries (Sheep).
Bukaryota, Metacoa; Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia; Butheria; Cetartiodactyla, Ruminantia; Pecora; Bovoidea; Bovidae; Caprinae; Ovis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 6; Length 98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92.4%; Score 158; DB 6; Length 98 90.3%; Pred. No. 1.4e-15; Live 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF450453; AAL47178.1; -.
SEQUENCE 98 AA; 10513 MW; 2A53331ED62CAABS CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALIGNMENTS
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QBKZ57
QBYWC7
QBFM14
Q9SD86
QBUKM3
                                                                                                                                                                                                                                              Q8PERO
Q91022
Q45375
O88002
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Q8G4X2
O33340
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Q8LMF7
Q8GSK7
Q8BJ19
 P74747
Q9L8J6
Q9GRAO
QBRTV7
QBNJX4
Q8FM04
                                                                                                          Q9EYB3
Q97A00
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                                                                                                          Q9W624 PRELIMINARY;
Q9W624;
01-NOV-1999 (TEMBLrel. 12,
01-NOV-1999 (TEMBLrel. 12,
01-DEC-2001 (TEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 90.3
nes 28; Conservative
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   Query Match
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Q8WN12;
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ID Q9
AC Q9
DT 01
DT 01
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006348 mycobacteri
004ku9 brassica ca
094f29 brassica ca
09a5e9 caulobacter
026276 methanobact
0303127 streptomyce
09ujf9 homo sapien
09da19 mus musculu
060687 homo sapien
08ww85 homo sapien
045883 eubacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9w624 carassius a
Q9ilw4 pseudomonas
O87474 burkholderi
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                                                                                                        December 3, 2003, 19:03:25; Search time 26.5 Seconds (without alignments) 301.873 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                            830525
                 GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                   171
1 SRTHRHSMEIRTPDINPAWYASRGIRPVGRF 31
                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                               830525 seqs, 258052604 residues
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                                                                             - protein search, using sw model
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Q9M624
Q91M4
Q87474
Q9M371
Q94K29
Q9AK29
Q9A
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1: Sp_archea:*
2: Sp_bacteria:*
3: Sp_tungi:*
1: Sp_tungi:*
1: Sp_tungi:*
1: Sp_tungi:*
1: Sp_mannal:*
1: Sp_mhc:*
1: Sp_mhc:*
1: Sp_phage:*
1: Sp_thage:*
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sp_virus:*
sp_vertebrate:*
sp_unclassified:*
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Gapop 10.0 , Gapext 0.5
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Q45883
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Maximum Match 100%
Listing first 45 su
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sp_bacteriap:*
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Maximum DB seq length: 200000000
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Match Length
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Perfect score:
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Gaps

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Result

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STRAIN=DNT;
MEDLITRE=91394809; PubMed=8449889;
Suen W.C., Spain J.C.;
Cloning and characterization of Pseudomonas sp. strain DNT genes for 2,4-dinitrotoluene degradation.";
J. 4-dinitrotoluene degradation.";
J. Bacteriol. 175:1831-1837(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota, Viridiplantae; Streptophyta; Embryophyta, Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Haigler B.E., Johnson G.R., Suen W.C., Spain J.C.;
"Biochemical and genetic evidence for meta-ring cleavage of 2,4,5-
trihydroxytoluene in Burkholderia sp. strain DNT.";
J. Bacteriol. 181-965-972 (1999).
EMBL, AR076848; AAD12738.1; -.
SEQUENCE 315 AA; 34745 MW; E99261179022961E CRC64;
                                          Burkholderia cepacia (Pseudomonas cepacia).
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Burkholderiacese; Burkholderia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    De Haan M., Maarse A.C., Grivell L.A., Mewes H.W., Lemcke K.,
Mayer K.F.X., Quetier F., Salanoubat M.;
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Match 32.2%; Score 55; DB 2; Length 315; Local Similarity 44.4%; Pred. No. 7.1; onservative 3; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09M371;
01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Hypothetical 87.4 kDa protein.
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            216 SRMTHCSFRIQDLDAQFLGNKWLASRGWKPGWGVGR 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 SRITHRHSMEIRIPD --- INPAWYASRGIRP --- VGR 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              366 PPHNPRTYGŚRGLOPHGRW 384
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                             Trihydroxytoluene oxygenase.
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hes 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=DNT;
MEDLINE=99121037;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9M371
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 5
Q9M371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
006348
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STRAIN=ATCC 15592 / PAO1;
MEDLINE=2047337; PubMed=10984043;
MEDLINE=20437337; PubMed=10984043;
Stover C.K., Pham F.L., Erwin A.L., Mizoguchi S.D., Warrener P.,
Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
Brody L.L., Coulter S.N., Folger K.R., Ka A., Larbig K., Lim R.M.,
Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
"Complete genome sequence of Pseudomonas aeruginosa PAO1, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                               Gapa
                                             Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Carassius.
NCBI_TaxID=7957;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
NCBI_TaxID=287;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33.0%; Score 56.5; DB 16; Length 664; 45.8%; Pred. No. 9.7;
                                                                                                                                                                                                                                                                                                                                                                                     ch 57.3%; Score 98; DB 13; Length 117; Il Similarity 53.8%; Pred. No. 1.1e-06; 14; Conservative 8; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                             Satake H., Minakata H., Fujimoto M.;
"Carassius RFamide (C-RF amide) ";
Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AB020024; BAA756652.1; - D5DC4CB22038C2B0 CRC64;
SEQUENCE 117 AA; 12879 MW; D5DC4CB22038C2B0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AR004642; AAG05539.1; -.
InterPro; IPR001589; Actbind actnin.
InterPro; IRR00604; Alpha amyl_cat.
Pfam; PF00128; alpha-amylase; 1.
PROSITE; PS00019; ACTNIN 1; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 664 AA; 76329 MW; 8FS9FEED54C308AD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            664 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         315 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 HSMEIRTPDINPAWYASRGIRPVGRF 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 HRHSMEIRTPDINPAWYASRGIRP 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                             Carassius auratus (Goldfish).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              O87474;
01-NOV-1998 (TrEMBLrel. 08,
01-NOV-1998 (TrEMBLrel. 08,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein PA2151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 45.8 es 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 opportunistic pathogen."
Nature 406:959-964(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pseudomonas aeruginosa.
                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
                                                                                                                                                                             SEQUENCE FROM N.A.
TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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087474
ID 0874
AC 0874
DT 01-N
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Q911W4

1D Q911W4

DT 01-M

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Gape

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ö Gaps ö 31.6%; Score 54; DB 10; Length 790; 52.6%; Pred. No. 27; Indels EU Arabidopsis sequencing project;
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, Al132959; CAB71097.1; -.
Hypothetical protein:
SEQUENCE 790 AA; 87376 MW; B222724B75690F30 CRC64; 9

à

Gaps

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Kim H.U., Wu S.S., Ratnayake C., Huang A.H.; Brassica rapa Has Three Genes That Encode Proteins Associated with
                                                                                                                                                            Different Neutral Lipids in Plastids of Specific Tissues.";
Plant Physiol. 126:330-341(2001).

EMBL, AR29053; AAK57561.1;
InterPro; IPR006843; Par fibrillin.
Pfam; PP04755; Par fibrillin; 1.

SEQUENCE 327 AA; 35678 MW; 8C7B87FCD6C02422 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                           1 31.0%; Score 53; DB 10; Length 327; Similarity 43.8%; Pred. No. 15; 7; Conservative 3; Mismatches 6; Indels
                                                                     MEDLINE=21249173; PubMed=11351096;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 HRHSMBIRTPDINPAW 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 43.8 Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           crescentus.
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Q9A5E9;
01-JUN-2001 (
01-JUN-2001 (
01-MAR-2003 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Caulobacter
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Best Local
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Matches
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999 PT 10 P
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         SURETTERE
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WEDLINES-9829987; PubMed=9634230;

Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,

Cole S.T., Brosch R., Falkhill J., Garnier T., Churcher C., Harris D.,

Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F.,

Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,

Badcock K., Basham D., Ercwh I., Gentles S., Hamlin N., Holroyd S.,

Hornsby T., Jagels K., Kroph A., McLean J., Moule S., Murphy L.,

Hornsby T., Jagels K., Kroph A., Rajandream M.A., Rogers J.,

Rutter S., Geeger K., Skelton S., Squares R.,

Sulston J.E., Taylor K., Whitchead S., Barrell B.G.;

"Deciphering the biology of Mycobacterium tuberculosis from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Brassica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRANN=CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Fleischmann R.D., Alland D., Eisen J.A., Earlon J., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Whole genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13;
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                                                                                                                                                                                                                                                                                   Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                     01-UUL-1997 (TrEMBLrel. 04, Created)
01-UUL-1997 (TrEMBLrel. 04, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical 33. 2 kDa protein (Oxidoreductase, short-chain dehydrogenase/reductase family).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00106; adh short; 1.
PROSITE; PS00061; ADH SHORT; 1.
Hypothetical protein; Oxidoreductase; Complete proteome.
SEQUENCE 314 AA; 33194 MW; 26144BA917E09274 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27
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      314 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            327 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; 295390; CABO8708.1; -.
EMBL; AE007162; AAK47948.1; ALT_INIT.
HSSP; P29132; 1DFI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-DEC-2001 (TrEMBLrel. 19, Created)
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                                                                                                                                                                                                                              OR MT3589 OR MTCY13E12.38C.
   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         fuberculist; Rv3485c; -.
InterPro; IPR002198; ADH short.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complete genome sequence.";
                                                                                                                                                                                                                                                            Mycobacterium tuberculosis
   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=1773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (SDR) FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=3711;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TIGR; MT3589;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tuberculist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bishai W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         187
                                                                                                                                                                                                                              RV3485C
006348
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094F29;
01-DEC-2001 (TERMELrel. 19, Created)
01-DEC-2003 (TERMELrel. 23, Last sequence update)
01-DEC-2003 (TERMELrel. 23, Last sequence update)
01-MAR-2003 (TERMELrel. 23, Last annotation update)
18 AR STANDER (Field mustard).
18 AR STANDER (Field mustard).
19 AR STANDER (Field mustard).
19 AR STANDER (Field mustard).
19 AR STANDER (Field mustard).
10 AR STANDER (Field mustard).
10 AR STANDER (Field mustard).
11 Brassicales, Brassicaceae; Brassica.
11 Brassicales, Brassicaceae; Brassica.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-21249173; PubMed=11351096; Kim H U., Wu S.S., Ratnayake C., Huang A.H.; Parasasica rapa Has Three Genes That Encode Proteins Associated with Different Neutral Lipids in Plaatids of Specific Tissues."; Plant Physiol. 126:330-341(2001).

EMBL; AR290566; AAK57564.1; -...

PIREL; PRO06843; PAP fibrillin.

PERM; PRO4755; PAP fibrillin; 1.

SEQUENCE 327 AA; 35644 MW; 6116E7F1B6C02C88 CRC64;
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Caulobacteraceae; Caulobacter.
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Sensory box histidine kinase/response regulator.
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STRAIN=ATCC 19089 / CB15;
MEDLINE=21173698; PubMed=11259647;
45 HRHDFKVRASDVNDEW 60
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PRT;
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37 AWWAAVLRGESGIRPVGRF 55
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hes 11, Conservative
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Matches 13; Conserv
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SEQUENCE 785 AA
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Matches
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Q93LZ7
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Q9UJF9
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Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,

A Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,

DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,

Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,

A Utterback T., Tran K., Holf A., Vamathevan J., Ermolaeva M., White O.,

A Salzberg S.L., Venter J.C., Shapiro L., Praser C.M.,

Complete genome sequence of Caulobacter crescentus.",

Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).

C -- SIMILARITY: TIEN V-TERMINAL REGION IS SIMILAR TO THAT OF OTHER

REGULATORY COMPONENTS OF SENSORY TRANSDUCTION SYSTEMS.

C -- SIMILARITY: TO PROKARYOTE SENSORY TRANSDUCTION PROTEINS.

R HSSP; Q56312; 3TMY.

R TIGR: CC2501; --
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PP00989; PAS; 1.

Pfam; PP00989; PAS; 1.

PFINITS: PR00072; response reg; 1.

PRINTS: PR00034; BCTRLSENSOR.

ProDom; PD000039; HATPase c; 1.

SMART; SM0038; Hiskx, 1.

SMART; SM00081; PAS; 1.

SMART; SM00091; PAS; 1.

SMART; SM00091; PAS; 1.

SMART; SM00091; PAS; 1.

TIGRFAMS; TIGR00229; sensory box; 1.

PROSITE; PS50109; HIS_KIN; 1.

PROSITE; PS50110; PAS; 1.

PROSITE; PS50110; PAS; 1.

RESPONSE REGULATORY; 1.
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Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
Methanobacteriaceae; Methanothermobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Match 31.0%; Score 53; DB 16; Length 637; Local Similarity 48.0%; Pred. No. 30; es 12; Conservative 4; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     637 AA; 68511 MW; 0EDEEAF76FFA8611 CRC64;
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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                                                                                                                                                                                                                                                                                                                         InterPro; IPR003594; Arbbind Arbase.
InterPro; IPR004358; Bact sens pr_C.
InterPro; IPR004567; His kinA.
InterPro; IPR005467; His kinase.
InterPro; IPR001610; PAC.
InterPro; IPR000100; PAS-assoc_C.
InterPro; IPR000110; PAS-domain.
InterPro; IPR00011789; Response_reg.
Pfam; PF02518; HATPase_C; 1.
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SEQUENCE 637 AA
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Matches
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A McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M.,
Dandels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.;
"Complete genome sequence of Methanobacterium thermoautotrophicum
deltaH: functional analysis and comparative genomics.";
J. Bacteriol. 179:7135-7155 (1997).

R RMBL, AR000805; Alaske60.1;
R Interpro; IPR00349; ATPDIA ATPARS.
RINTERPO; IPR004515; BPD_transp.
R Interpro; IPR004615; BPD_transp.
R Interpro; IPR004610; PAC.
R Interpro; IPR00010; PAS-assoc_C.
R Interpro; IPR00010; PAS-assoc_C.
R R Pfam; PF00518; HATPARS domain.
R Pfam; PF00785; PAC; 1.
R Pfam; PF00785; PAC; 1.
SMART; SM0086; PAC; 1.
R SMART; SM0086; PAC; 1.
R SMART; SM0086; PAC; 1.
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EMBL; AX033994; AAK6179.1; -.
HSSP; P39435; 1B3N.
InterPro; IPR00794; Ketoacyl-synt.
Pfam; PF00109; ketoacyl-synt.
Pfam; PF00109; ketoacyl-synt.
SEQUENCE 420 AA; 43011 MW; 3C27E22BE88C2DEA CRC64;
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46.4%; Pred. No. 53;
tive 1; Mismatches 12; Indels
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1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
Chain length factor-like protein.
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PROSITE; PS00402; BPD_TRANSP_INN_MEMBR; 1.
PROSITE; PS50109; HIS_KIN; 1.
PROSITE; PS50113; PAC; 1.
PROSITE; PS50112; PAC; 3.
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Gaps

9

Indels

8;

2; Mismatches

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14; Conservative
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 Matches
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                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hayashizaki Y.; "Functional annotation of a full-length mouse cDNA collection.";
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Pred. No. 41;
                                                                                                                                                                                                                                                                                     Length 54;
                                                                                                                                                                                                                                                                                                                  7; Indels
                                                                                                                                                                                             Lawlor S.;
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AL035608; CAB55682.1; -.
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EMBL; AKO06260; BAB24488.1; -.

MGD; MG1:1914185; 1700023B02Rik.

InterPro; PRO00345; CytC heme_bind.

PROSITE; PSO0190; CYTCCHRÖME C; 1.

SEQUENCE 450 AA; 51852 MW; P32F11BE6D6A4EAC CRC64;
                                                                                                                                                                                                                                                       54 AA; 6110 MW; E2F3C39F7B961A9F CRC64;
                     01-MAY-2000 (TTEMBLrel. 13, Created)
01-MAY-2000 (TTEMBLrel. 13, Last sequence update)
01-MAY-2000 (TTEMBLrel. 13, Last annotation update)
01-MAY-2000 (TTEMBLrel. 13, Last annotation update)
DJ479571.3 (Sushi-repeat protein (SRPUL)) (Fragment)
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (TrEMBLrel. 17, Last sequence update) (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                 29.8%; Score 51; DB 4; 50.0%; Pred. No. 4; tive 1; Mismatches
 54 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                      450 AA
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MEDLINE-21085660; PubMed-11217851;
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                                                                                                                                                                                                                                                                                                                                                                            18 TPAVTPTWYAGSGYYP 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                              12 TPDINPAWYASRGIRP
                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1700023B02Rik protein.
                                                                                                                                                                                                                                                                                                 Local Similarity
Les 8; Conserv
                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
                                                                                                                                             NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1700023B02RIK.
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                                                                                                                                                                                                                                                       SEQUENCE
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                                                                                                                                                                                                                                                                                     Query Match
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Q9DA19;
 Q9UJF9
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Matches
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Best Local Similarity

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Huang C.-H., Chen H., Peng J., Chen Y.;

"Cloning and characterization of the sushi-repeat containing protein
(SRP) as a novel interaction partner of Rh type C glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sushi-repeat protein.
Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
Kurosawa H., Inukai T., Inaba T., Goi K., Chang K.-S., Sinjyo T.,
Rakestraw K.M., Naeve C.W., Look T.A.;
Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29.8%; Score 51; DB 4; Length 465; 50.0%; Pred. No. 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strausberg R.;
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC020733; AAH20733.1; -.
InterPro; IPR001128; Cytochrome_P450.
InterPro; IPR003410; Hyalin.
InterPro; IPR000436; Sushi_SCR_CCP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (JUN-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                        01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Sushi-repeat protein (Sushi-repeat containing protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4D752B187FF3BFB8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         465 AA
                       373 SRSHRHSPEKKGSDRN-----RGIRSRSR 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 42;
1; Mismatches
1 SRITHRHSMEIRTPDINPAWYASRGIRPVGR 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL, AF060567; AACL5765.1; -... EMBL, AF393649; AAM73693.1; -... Interpro; IPR001128; Cytochrome_P450. Interpro; IPR003410; Hyalin. Interpro; IPR000436; Sushi_SCR_CCP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
                                                                                                                                          PRT;
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                                                                                                                                                                                   01-AUG-1998 (TrEMBLrel. 07, 01-AUG-1998 (TrEMBLrel. 07, 01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2002 (TrEMBLrel. 20,
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Best Local Similarity
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TISSUE=Placenta;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted
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DR Pfam; PF00084; sush1; 3.

DR SMART; SM00032; CCP; 3.

DR PROSITE; PS00086; CYTOCHROME_P450; 1.

SQ SEQUENCE 465 AA; 52957 MW; 3D7229487DA1B8BD CRC64;

Query Match
Best Local Similarity 50.0%; Pred. No. 42;

Matches 8; Conservative 1; Mismatches 7; Indels

QY 12 TPDINPAWYASRGIRP 27

| | | | | | | | | |

Db 18 TPAVTPTWYAGSGYYP 33
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0; Gaps

Search completed: December 3, 2003, 19:14:02 Job time: 27.5 secs

Prolactin releasin Prolactin releasin Rat PrRP-31 peptid Human PrRP-31 peptid Peptide production Peptide production Peptide production Human type G prote Rat type G protein Rat coxytocin secre

Rat CRH releasing Human CRH releasin Prolactin releasin

19P2 ligand peptid 19P2 ligand peptid

Peptide production Peptide production Human type G prote Rat type G protein Rat oxytocin secre

Human oxytocin sec Rat CRH releasing Human CRH releasin

Human oxytocin sec Rat CRH releasing Human CRH releasin

Peptide production Peptide production Murine pituitary-d Rat type G protein Rat type Ligand po Rat oxytocin secre Rat CRH releasing

Новоуа М;

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2 M 4 M 9 F 8 9

Result

OM protein

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Run

Sequence:

Minimum DB Maximum DB

Database

Searched:

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G protein-coupled receptor; ligand binding; pharmaceutical;
modulator; pituitary; central nervous system; pancreas; prophylactic;
therapeutic, agent.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       ALIGNMENTS
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                                                                                          AAB90995
AAE26400
                                                                                                               AAE26401
ABU60826
ABU60827
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AAW31392
AAW31385
AAB10356
AAB10363
AAG62525
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AAW31393
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AAB10364
AAG62526
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AAB10354
AAG62523
                                                       AAB90991
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ABU60845
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AAW31383
                                                                                                                                                                                                                                          ABU60838
                                                                                                                                                                                                                                                                            AAW31386
                                             AAG62524
                                                                               PAB90993
                                                                                                                                                ABU60837
                                                                                                                                                                                                                                                                                                                         AAG62533
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95JP-0343371.
96JP-0059419.
96JP-0211805.
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 TAKE ) TAKEDA CHEM IND LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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f, Kitada C;
Pujii R, Pul
Kawamata Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WQ9724436-A2
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15-MAR-1996;
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147
147
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 RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human type G prote
Rat type G protein
Rat type Ilgand po
Human type ligand.
Rat 19P2 ligand.
Human 19P2 ligand.
Murine pituitary-d
Murine pituitary-d
Rat oxytocin secre
                                                                         December 3, 2003, 18:57:14; Search time 33.75 Seconds (without alignments) 145.793 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                             A Geneseq 19Jun03:*

| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
| SIDSI/gcgdata/geneseqg/geneseqp-embl/AA1981.DAT:*
| SIDSI/gcgdata/geneseqg-embl/AA1981.DAT:*
| SIDSI/gcgdata/geneseqg-embl/AA1981.DAT:*
| SIDSI/gcgdata/geneseqg-embl/AA1983.DAT:*
| SIDSI/gcgdata/geneseqg-embl/AA1985.DAT:*
| SIDSI/gcgdata/geneseqg-embl/AA1985.DAT:*
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| SIDSI/gcgdata/geneseqg-embl/AA1980.DAT:*
| SIDSI/gcgdata/geneseqg-embl/AA1980.DAT:*
| SIDSI/gcgdata/geneseqg/emble-embl/AA1980.DAT:*
| SIDSI/gcgdata/geneseqg/emble-embl/AA1980.DAT:*
| SIDSI/gcgdata/geneseqg/emble-embl/AA1980.DAT:*
| SIDSI/gcgdata/geneseqg/emble-embl/AA1990.DAT:*
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                                                                                                                                                                                                                              1107863
           5.1.6
Compugen Ltd.
                                                                                                                                                1 SRXHXHSMEXRTPDINPAWYXXRGIRPVGRP 31
                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                        1107863 seqs, 158726573 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUMMARIES
           GenCore version (c) 1993 - 2003
                                                                                                                                                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                      - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW31391
AAW31384
AAW97233
AAW97235
AAW87614
AAW87615
AAW95173
AAW95173
AAW95173
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seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Copyright
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Title:
Perfect score:
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7447
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                                                                                               This sequence represents a peptide fragment from a novel human type
ligand polypeptide corresponding to amino acid residues 23 to 53 of the
sequence represented in AAM3130 and is used in an assay to monitor
ligand binding to the G protein-coupled receptor protein. Pharmaceutical
compositions containing this ligand may be used as a pituitary function
modulator, a central nervous system modulator or a pancreatic function
modulator. This ligand could have specific applications as a
prophylactic or therapeutic agent for dementia, depression, hyperkinetic
prophylactic or therapeutic agent for dementia, depression, hyperlyindactic or therapeutic agent for dementia, depression, hyperlyindactic or therapeutic agent for dementia, depression, hyperlyindacmia, epilepsy, amylotrophic lateral sclerosis,
cute myocardial infarction, infertility, spinocerebellar degeneration,
cute myocardial infarction, infertility, spinocerebellar degeneration,
coligogalactia, Assays can also be developed to screen compounds which are
capable of altering the binding activity of the ligand affecting
activation of the G protein-coupled receptor protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           G protein-coupled receptor; ligand binding; pharmaceutical;
modulator; pituitary; central nervous system; pancreas; prophylactic;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                      Ligand peptide for G protein-coupled receptor - acts by modulating function in the central nervous system, pancreas and pituitary gland
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rat type G protein-coupled receptor ligand fragment 1.
                                                                                                                                                                                                                                                                                                                                                                                                   95.5%; Score 147; DB 18;
83.9%; Pred. No. 3.3e-17;
iive 0; Mismatches 5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 SRXHXHSMEXRTPDINPAWYXXRGIRPVGRF 31
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                                                                             Claim 2; Page 184; 258pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW31384 standard; Peptide; 31 AA
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96JP-0211805.
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                                                                                                                                                                                                                                                                                                                                                                                                                                 26; Conservative
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Kawamata Y, Kitada C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1997-363672/33.
N-PSDB; AAV02421.
WPI; 1997-363672/33.
N-PSDB; AAV02428.
                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     therapeutic agent
                                                                                                                                                                                                                                                                                                                                                                            31 AA;
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12-AUG-1996;
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28-DEC-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10-JUL-1997
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                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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This sequence represents a peptide fragment from a novel rat type
ligand polypeptide corresponding to amino acid residues 22 to 52 of the
equence represented in AAMISIS and is used in an assay to monitor
ligand binding to the G protein-coupled receptor protein. Pharmaceutical
ligand binding to the G protein-coupled receptor protein. Pharmaceutical
compositions containing this ligand may be used as a pituitary function
modulator. A central nervous system modulator or a pancreatic function
modulator. This ligand could have specific applications as a
prophylactic or therapeutic agent for dementa, depression, hyperkinetic
syndrome, disturbance of consciousness, anxiety syndrome, schizophrenia,
trauma, growth hormone secretory disease, hyper- and polyphagia,
hyperlipidaemia, hypercholesterolaemia, hypersjyceridaemia,
hyperlipidaemia, diabetes, cancer, pancreatitis, renal disease,
hyperlipidaemia, asthma, rhemmatoid arthritis, spinal injury,
translent brain ischaemia, epilepsy, amylotrophic lateral sclerosis,
cute myocardial infarction, infertility, spinocerebellar degeneration,
coligogalactia. Assays can also be developed to screen compounds which are
capable of altering the binding activity of the ligand affecting
activation of the G protein-coupled receptor protein.
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Ligand peptide for G protein-coupled receptor - acts by modulating function in the central nervous system, pancreas and pituitary gland
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95.5%; Score 147; DB 18; 83.9%; Pred. No. 3.3e-17; ive 0; Mismatches 5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 SRXHXHSMEXRTPDINPAWYXXRGIRPVGRP 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SRAHOHSMETRTPDINPAWYTGRGIRPVGRF 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rat type ligand polypeptide fragment.
                                                                                                                Claim 2, Page 179, 258pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW97233 standard; peptide; 31 AA
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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Matches
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1 SRXHXHSMEXRIPDINPAWYXXRGIRPVGRF 31
                                                                                                                                                                              1 SRAHQHSMETRTPDINPAWYTGRGIRPVGRF 31
                                                                                                                                                                                                                                            Human type ligand polypeptide fragment.
                                                                                                                                                                                                                                                                                                        abnormal lipidmetabolism; oxytocia
                          Claim 3; Page 153; 241pp; English
                                                                                                                                                                                                            AAW97235 standard; peptide; 31 AA
                                                                                                                                                                                                                                                                                                                                                                                   Kawamata Y,
                                                                                                                                                                                                                                                                                                                                                   98WO-JP02765.
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                                                                                                                                                            26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                   Fujii R, Hinuma S,
                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1999-105614/09.
                                                                                                                                                      Local Similarity
                                                                                                                                      31 AA;
                                                                                                                                                                                                                                                                                                                            WO9858962-A1
                                                                                                                                                                                                                                                                                                                                                   22-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                             23-JUN-1997;
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                                                                                                                                      Sequence
                                                                                                                                                                                                                       AAW97235;
                                                                                                                                                Query Match
                                                                                                                                                           Matches
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The present sequence represents a human type ligand fragment. It is used in the course of the invention. The specification describes an agent condulating prolactin secretion which comprises a ligand polypeptide or a salt, for a G protein-coupled receptor (GPCR) protein. The agents for promoting prolactin secretion can be used for treating or preventing hypocoarianism, gonecyst cacogenesis, menopausal syndrome, euthyroid or hypometabolism. They can by used for promoting lactation in a domestic mammal and as an aphrodisiac. The agents for inhibiting prolactin secretion can be used for treating or preventing pluttery adenomatosis, brain tumour, emmeniopathy, autoimmune disease, prolactinoms, infertility, impotence, amenorrhea, galactorrhea, cornegaly, chiari-frommel syndrome, lymphoma, Sheehan syndrome or dyszoospermia. The inhibitory agents can also be used as contraceptives. The agents for modulating placental function can be used for treating or preventing choricearcinoma, hydatid mole, itruption mole, abortion, unthirity fetus, abnormal saccharometabolism, abnormal lipidmetabolism or oxytocia. Use of G protein-coupled receptor ligands - for modulating prolactin secretion or placental function, e.g. for treating menopausal syndrome, tumours, autoimmune disease or abnormal pregnancy Producing a 19P2 pituitary G protein receptor ligand - by cleavar of a fusion protein, useful for preventing and treating dementia, breast cancer, renal failure and autoimmune disease Length 31; 19P2 ligand, G protein coupled receptor; pituitary; prolactin releasing peptide; rat; dementia; breast cancer; 5; Indels 95.5%; Score 147; DB 20; 83.9%; Pred. No. 3.3e-17; Tanaka Y; 1 SRXHXHSMEXRTPDINPAWYXXRGIRPVGRF 31 0; Mismatches Moriya T, Nishimura O, Suenaga M, Claim 3; Page 159; 241pp; English AAW87614 standard; Peptide; 31 98BP-0111725. (TAKE ) TAKEDA CHEM IND LTD (first entry) Best Local Similarity 83.5 Matches 26; Conservative WPI; 1999-047884/05. 31 AA; Rat 19P2 ligand. 25-JUN-1998; 27-JUN-1997; 29-MAR-1999 BP887417-A2. 10-DEC-1998 Rattus sp. Sequence AAW87614; Query Match therapy. RESULT 5 AAW87614 %\$CGGGGGGGGGGGGGGGGGG ö choriocarcinoma, hydatid mole, irruption mole, abortion, unthrifty fetus, abnormal saccharometabolism, abnormal lipidmetabolism or oxytocia. pituitary adenomatosis, brain tumour, emmeniopathy, autoimmune disease, prolactinoma, infertility, impotence, amenorrhea, galactorrhea, cromegaly, Chiarti-Frommel syndrome, Argonz-del Castilo syndrome, Forbes-Albright syndrom, lymphome, Sheehan syndrome or dyszoospermia. The inhibitory agents can also be used as contraceptives. The agents for modulating placental function can be used for treating or preventing Rat type ligand; modulation; prolactin secretion;

G protein-coupled receptor; GPCR; hypocvarianism; gonecyst cacogenesis;
menopausal syndrome; euthyroid; hypometabolism; lactation;
pituitary adenomatosis; brain tumour; emmeniopathy; autoimmune disease;
prolactinoma; infertility; impotence; amenorrhea; galactorrhea;
acromegaly; Chiari-Frommel syndrome; Argonz-del Castilo syndrome;
Porbes-Albright syndrome; lymphoma; Sheehan syndrome; dyszoospermia;
contraceptive; placental function; choriccarcinoma; hydatid mole;
irruption mole; abortion; unthrifty fetus; abnormal saccharometabolism; The present sequence represents a rat type ligand fragment. It is used in the course of the invention. The specification describes an agent for modulating prolactin secretion which comprises a ligand polypeptide or a salt, for a G protein-coupled receptor (GPCR) protein. The agents for promoting prolactin secretion can be used for treating or preventing hypovarianism, gonecyst cacogenesis, menopausal syndrome, euthyroid or hypometabolism. They can by used for promoting lactation in a domestic mammal and as an aphrodisiac. The agents for inhibiting prolactin secretion can be used for treating or preventing Use of G protein-coupled receptor ligands - for modulating prolactin secretion or placental function, e.g. for treating menopausal syndrome, tumours, autoimmune disease or abnormal pregnancy Gaps ö Length 31; 5; Indels 95.5%; Score 147; DB 20; 83.9%; Pred. No. 3.3e-17; iive 0; Mismatches 5;

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Gaps

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by cleavage

This is the amino acid sequence of the rat pituitary G protein-coupled receptor ligand 19P2L. A method suitable for

Claim 5; Page 34; 56pp; English.

Matsumoto H;

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         commercial inginatever production of 1972 completes the complete of the commercial ingination has cells as a recombinant fusion process, with human basic fibroblast growth factor (see AAV8394-95) that has been modified to include an N-terminal cysteine residue. The ligand is released from the fusion by cyanylation followed by amonolysis. 1972L has prolactin secretion-inhibiting properties. It can be used in the treatment and prevention of various diseases including sendle dementia, cerebrovascular dementia, and dementia associated with: genealogical disorders (e.g. Alzahemer's disease, Parkinson's disease, Pick's disease, Huntingron's disease), infectious disease to train contaction by drugs, metal and organic compounds), tumourigenic diseases (e.g. Creutzfeldt-Jakob's), endocrine or metabolic disease or toxicosis (e.g. brain tumour), traumatic diseases (e.g. chronic diseases (e.g. brain tumour), traumatic diseases (e.g. chronic diseases (e.g. brain tumour), traumatic diseases (e.g. chronic diseases associated with prolactin hypo and hypersecretion consciousness. It is also useful for prevention and treatment of these transfer disease associated with prolactin hypo and hypersecretion respectively, including: hyperprolactinaemia, pituitary adenoma, breast cancer, infertility, impotence and autoimmune disease (hypersecretion disorders). The 19P2 polypeptide/amide is also useful as a test creagent for study of the prolactin secretory function or as a readent for study of the prolactin secretory function or as a
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commercial high-level production of 19P2L comprises expressing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19P2 ligand, G protein coupled receptor; pituitary; prolactin releasing peptide; human; dementia; breast cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 147; DB 20; Length 31;
Pred. No. 3.3e-17;
0; Mismatches 5; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 SRXHXHSMEXRTPDINPAWYXXRGIRPVGRF 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 SRAHQHSMETRIPDINPAWYTGRGIRPVGRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      lactogogue in mammalian farm animals.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW87615 standard; Peptide; 31 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1999-047884/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31 AA;
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AAW87615
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Claim 5; Page 35; 56pp; English

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Pituitary-derived ligand polypeptide; G-protein coupled orphan receptor; GPR10; UHR-1; modulator; pituitary; central nervous system; pancreas; tissue; screen; therapeutic; binding; senile dementia; ligand; murine; Alzheimer's disease; Parkinson's disease; Huntington's disease; drug; Creutzfeld-Jakob disease; poisoning; schizophrenia; growth hormone; secretion; diabetes; cancer; rheumatoid arthritis; epilepsy; vasopressor;
    This is the amino acid sequence of the human pituitary G
protein-coupled receptor ligand 19P2L. A method suitable for
commercial high-level production of 19P2L comprises expressing
the ligand in hose cells as a recombinant fusion protein e.g. with
human basic fibroblast growth factor (see AAV83796-97) that has
been modified to include an N-terminal cysteine residue. The
ligand is released from the fusion by cyanylation followed by
ammonolysis. 19P2L has prolactin secretion-stimulating and (at
high doses) prolactin secretion-inhibiting properties. It can be
used in the treatment and prevention of various diseases including:
entile dementia, cerebrovascular dementia, and dementia associated
with: genealogical disorders (e.g. Alzheimer's disease, Parkinson's
disease, pick's disease, Huntington's disease), infectious diseases
(e.g. Creutzfeldt-Jakob's), endocrine or metabolic disease or
confocials (e.g. brain tumour), traumatic diseases (e.g. chronic
diseases (e.g. brain tumour), traumatic diseases (e.g. chronic
chiseases (e.g. brain tumour), traumatic diseases (e.g. chronic
diseases (e.g. brain tumour), traumatic diseases (e.g. chronic
diseases (e.g. brain tumour), propes of dementia, depression,
hyperactive child syndrome (microencephalopathy) and disturbance of
consciousness: It is also useful for prevention and treatment of
diseases associated with prolactin hypo and hypersecretion
respectively, including: hypotence and autoimmune disease
(hypersecretion disorders), and seminal purhance of
corespectively, including: and seminal purhance of
the espectively independents), and seminal purhance of
consciousness in disorders), and seminal purhance of
consciousness and seminal syndrome and seminal purhance of
the espectively independents) and seminal purhance of
consciousness and seminal syndrome disease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       osteoporosis, menopausal syndrome and renal failure (hyposecretion disorders). The 19P2 polypeptide/amide is also useful as a test reagent for study of the prolactin secretory function or as a lactogogue in mammalian farm animals.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Murine pituitary-derived ligand mature polypeptide sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95.5%; Score 147; DB 20; 83.9%; Pred. No. 3.3e-17; ive 0; Mismatches 5
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hes 26, Conservative
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This represents the matured murine pituitary-derived ligand polypeptide sequence. The polypeptide is a ligand for the G-protein coupled orphan ceceptor designated GPR10 (human) or UHR-1 (rach). Cells transformed with a vector containing the ligand polypeptide. The ligand polypeptide are used to produce a recombinant ligand polypeptide. The ligand polypeptide, and its fragments, modulate function of the pituitary, central nervous system, pancreas and other tissues and can be used to sereen for agents that modulate binding of the polypeptide to the receptor; to quantify the amount of receptor in a sample and to raise antibodies. They may also be used therapeutically, e.g. to treat senile dementia, Alzhahaer's, Parkinson's or Huntington's diseases; Crentzfeld-Jakob disease; poisoning by heavy metals or drugs; diabetes; schizophrenia; disorders of growth cormone secretion; cancer; rheumatoid archritis, epilepsy and many others, also to improve post-operative nutritional status and as vasopressor. Transgenic animals carrying the ligand polypeptide encoding DNA or its mutein are used to study the function of the polypeptide.

Corpressing genes, as models of disease, for drug screening and as source of cell lines. The ligand polypeptide DNA is used as a source of probes and primers; to identify related sequences; in receptor-binding assays;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GPR10; UHR-1; modularor; pituitary; central nervous system; pancreas; tissue; screen; therapeutic; binding; senile dementa; ligand; murine; Alzheimer's disease; Parkinson's disease; Huntington's disease; drug; Creutzfeld-Jakob disease; polsoning; schizophrenia; growth hormone; secretion; diabetes; cancer; rheumatoid arthritis; epilepsy; vasopressor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pituitary-derived ligand polypeptide; G-protein coupled orphan receptor;
                                        polypeptide ligand for orphan G protein coupled receptors - treating disorders of central nervous system, pituitary and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Murine pituitary-derived ligand polypeptide antigenic epitope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 31;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95.5%; Score 147; DB 20;
83.9%; Pred. No. 3.3e-17;
ive 0; Mismatches 5;
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                                                                                                                       Disclosure; Page 134; 206pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW95174 standard; Protein; 31 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and to develop transgenic animals
                                                                                 pancreas, and for drug screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98WO-JP01923.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10-MAR-1999 (first entry)
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WPI; 1999-009423/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31 AA;
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Gaps

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The invention relates to a murine pituitary-derived ligand polypeptide which is a ligand for the G-protein coupled orphan receptor designated GPR10 (human) or UHR-11 (rat). Cells transformed with a vector containing the ligand polypeptide encoding DNA are used to produce a recombinant to the ligand polypeptide. The ligand polypeptide, and its fragments, modulate function of the pituitary, central nervous system, pancreas and other cissues and can be used to screen for agents that modulate binding of the polypeptide to the receptor; to quantify the amount of receptor in a sample and to ratise antibodies. They may also be used therapeutically, e.g. to treat senile dementia, Alzheimer's, Parkinson's or Huntington's diseases; Creutzfeld-Jakob disease; poisoning by heavy metals or drugs; creutzfeld-Jakob disease; poisoning by heavy metals or drugs; creumatoid arthritis, epilepsy and many others, also to improve post-coperative nutritional status and many others, also to improve post-coperative nutritional status and man vasopressor. Transgenic animals carrying the ligand polypeptide-expressing genes, as models of disease, for drug screening and as source of cell lines. The ligand colypeptide source of cell lines. The ligand cantisers, in drug development; for gene therapy and to develop creatises Amisch can tisers, in drug development; for gene therapy and to develop artisers, in drug developments artisers and to development antigent between the preparation of anti-ligand polypeptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rat; oxytocin secretion promoter; G protein-coupled receptor protein; treatment; disease; pain; atonic bleeding; uterine recovery failure; cow; caesarean section; artificial fertilization; galactostasis; goat; pig;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                          used
                                 New polypeptide ligand for orphan G protein coupled receptors -
for treating disorders of central nervous system, pituitary and
pancreas, and for drug screening
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    y Match 95.5%; Score 147; DB 20; Length 31; Local Similarity 83.9%; Pred. No. 3.3e-17; hes 26; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rat oxytocin secretion promoting peptide SEQ ID NO: 18.
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                                                                                                                               Disclosure; Page 26; 206pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB10355 standard; peptide; 31 AA
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WPI; 1999-009423/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31 AA;
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WPI; 2000-452298/39

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This invention describes a novel oxytocin secretion-regulating agent which contains a ligand peptide or its salt for the G protein-coupled receptor protein. It is useful in the form of drugs for ameliorating, preventing and treating diseases relating to oxytocin secretion e.g. weak pains and atonic bleeding, before and after expulsion of placenta, uterine recovery failure, caesarean section, stoppage of artificial fertilization or galactostasis and is also applicable in veterinary medicine for promoting milk production in cow, goat and pig. This sequence represents a rat peptide which acts as an oxytocin secretion
                    Physiologically-active polypeptide recognized as ligand by G protein-coupled receptor protein, for promoting secretion of oxytocin, as drugs for diseases relating to oxytocin secretion and in veterinary
                                                                                                                                                  Claim 3; Page 57; 72pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                  promoter
                                                                                                   medicine
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Length 31; Indels Score 147; DB 21; Pred. No. 3.3e-17; 0; Mismatches 5; 31 SRAHQHSMETRTPDINPAWYTGRGIRPVGRF SRXHXHSMEXRTPDINPAWYXXRGIRPVGRF 95.5%; 83.9%; Local Similarity 83.9 es 26, Conservative Query Match Matches ద ⋧

31 AA;

Sequence

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Gaps

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AAB10362 standard, peptide, 31 AA AAB10362; RESULT 10 AAB10362 

(first entry) 24-NOV-2000

Human, oxytocin secretion promoter, G protein-coupled receptor protein, treatment, disease, pain, atonic bleeding, uterine recovery failure, cow, caesarean section, artificial fertilization, galactostasis, goat, pig; Human oxytocin secretion promoting peptide SEQ ID NO: 32.

veterinary medicine; milk production,

Homo sapiens.

WO200038704-A1 06-JUL-2000.

99WO-JP07199 22-DEC-1999;

98JP-0369585, 25-DEC-1998; (TAKE ) TAKEDA CHEM IND LTD

Hinuma Kitada C, Matsumoto H,

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WPI; 2000-452298/39

Physiologically-active polypeptide recognized as ligand by G protein-coupled receptor protein, for promoting secretion of oxytocin, as drugs for diseases relating to oxytocin secretion and in veterinary medicine

Disclosure; Page 62; 72pp; Japanese

This invention describes a novel oxytocin secretion-regulating agent which contains a ligand peptide or its salt for the grotein-coupled receptor protein. It is useful in the form of drugs for ameliorating, preventing and treating diseases relating to oxytocin secretion e.g. weak pains and atonic bleeding, before and after expulsion of placenta,

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uterine recovery failure, caesarean section, stoppage of artificial fertilization or galactostasis and is also applicable in veterinary medicine for promoting milk production in cow, goat and pig. This sequence represents a human peptide which acts as an oxycocin secretion
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                                                                                                                      21; Length 31;
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                                                                                                                     Score 147; DB 21;
Pred. No. 3.3e-17;
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                                                                                                                                                   0; Mismatches
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                                                                                                                  95.5%;
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Best Local Similarity
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Matches
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Prolactin-releasing peptide; PrRP; GPR10; G protein-coupled receptor; feeding behaviour; food intake; modulation; antagonist; anorectic; obesity; agonist; cachexia. Rat prolactin-releasing peptide, PrRP. (first entry) 18-JUL-2000 AAY87504; AAX87504

IIID AAX8

AAX

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AAY87504 standard, protein, 31

/note= "C-terminal amide" Location/Qualifiers Key Modified-site Rattus sp.

WO200017641-A1 30-MAR-2000 99WO-US21243 22-SEP-1999;

98US-0101380. 98US-0172353. 22-SEP-1998; 14-OCT-1998; (MILL-) MILLENNIUM PHARM INC.

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Stricker-Kongrad A,

WPI, 2000-303231/26

Identifying modulators of body weight by a combination of a cell-free or cell-based assay to identify modulators of GPR10, followed by an in vivo assay for the compounds effect on e.g. feeding behavior -

Example 2; Page 61; 82pp; English.

The invention relates to a method for identifying compounds useful for modulating body weight. The method comprises cell-free and/or cell-based assays that identify compounds which bind to and/or activate or inhibit the activity of GPR10, a G protein-coupled receptor. These assays are then followed by an in vivo assay of the effect of the compound on releasing peptide (PrRP; AAV87504) is a ligand of GPR10. Binding of PRR to GRR10 stimulates a signal transduction cascade, which results in an increase in food intake. Compounds identified using the method of the invention are useful for the modulation of body weight. Antagonists of GPR10 can be used to treat obesity, while GPR10 agonists can be used to treat sequence represents rat PrRP.

31 AA; Sequence

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antibody; 19P2 ligand; diagnosis; prolactin secretion; regulatory mechanism; central nervous system; pancreatic.
                                                                                                                                                                                                                                                                                                                                                                 New monoclonal antibodies, useful in diagnosis, as drugs and studying diseases related to ligand abnormality
                                                                                                                                                     /note= "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure, Page 26; 73pp; Japanese.
                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                               Matsumoto H, Kitada C, Hinuma S;
                                     19P2 ligand peptide fragment.
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             22-FEB-2000 (first entry)
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Modified-site
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                                                               Monoclonal
                                                                           pituitary;
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                                                                                                     Rattus sp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention provides a monoclonal antibody which has a specific reaction with the part peptide of the C-terminal of 19P2 ligand or its derivative. The antibodies can be used in diagnosis or to treat or prevent diseases associated with abnormality in the pituitary function regulatory mechanism (e.g. promotion of prolactin secretion), central nervous regulatory mechanism, and pancreatic function regulatory mechanism, and pancreatic function regulatory mechanism. The antibody-based immunoassay can also be applied in clarifying the physiological functions of the ligand and its derivative. Sequences AAY49290-302 represent peptide fragments of the 19P2 ligand.
                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                              Monoclonal antibody, 19P2 ligand; diagnosis; prolactin secretion, pituitary; regulatory mechanism; central nervous system; pancreatic.
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Query Match 95.5%; Score 147; DB 21; Length 31; Best Local Similarity 83.9%; Pred. No. 3.3e-17; Matches 26; Conservative 0; Mismatches 5; Indels
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                                                   1 SRXHXHSMEXRIPDINPAWYXXRGIRPVGRF 31
                                                                    1 SRAHQHSMBTRTPDINPAWYTGRGIRPVGRF 31
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                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                           AAY49291 standard; peptide; 31 AA
                                                                                                                                                                                                                      19P2 ligand peptide fragment
                                                                                                                                                                                                                                                                                                                                                                                                                      99WO-JP02650
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derivative
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The invention provides a monoclonal antibody which has a specific reaction with the part peptide of the C-terminal of 19P2 ligand or its derivative. The antibodies can be used in diagnosis or to treat or prevent diseases associated with abnormality in the pituitary function regulatory mechanism (e.g. promotion of prolactin secretion), central nervous regulatory mechanism, and pancreatic function regulatory mechanism, and pancreatic function regulatory mechanism. The antibody-based immunosssay can also be applied in clarifying the physiological functions of the ligand and its derivative Sequences AAY49290-302 represent peptide fragments of the 19P2 ligand.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 SRXHXHSMEXRIPDINPAWYXXRGIRPVGRF 31
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AAY49292 standard; peptide; 31 AA

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                                                                                                                                                                                                                        The present sequence describes a method of controlling the secretion of corticotrophin releasing hormone (CRH), involving the use of a G protein receptor This can be used to control the secretion of CRH and is useful as an analgesic or for treating, preventing or ameliorating diseases associated with CRH secretion such as hyperaldosteronism, hypercortisolaemia, secondary or chronic hypodremocorticism, Addison's disease (including boredom, nauses, pigmentation, hypogonadism, hair loss, and hypotension), adrenal gland hypofunction and obesity. The present sequence is a peptide used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human, corticotrophin releasing hormone; CRH; G protein receptor ligand; analgesic; hyperaldosteronism; hypercortisolaemia; hypoadrenocorticism; Addison's disease; adrenal gland hyperfunction; obesity.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Gape
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                                                                                                                                                          Use of G protein receptor ligand or peptide for controlling corticotropin releasing hormone secretion -
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                                                                                                                                                                                                                                                                                                                                                                                                     Length 31;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                   ch 95.5%; Score 147; DB 22; 1
1 Similarity 83.9%; Pred. No. 3.3e-17;
26; Conservative 0; Mismatches 5;
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                                                                                                                                                                                                   Claim 3; Page 69; 90pp; Japanese
                                                                                                        Kitada C, Matsumoto H, Hinuma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hinuma
                                       18-NOV-1999; 99JP-0327900.
26-SEP-2000; 2000JP-0297073.
             17-NOV-2000; 2000WO-JP08119.
                                                                              (TAKE ) TAKEDA CHEM IND LID
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26-SEP-2000; 2000JP-0297073
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24-AUG-2001 (first entry)
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                                                                                                                                WPI; 2001-355552/37
                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                             31 AA;
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                                                                                                                                                                                                                                                                                                                                                    invention
                                                                                                                                                                                                                                                                                                                                                                             Sequence
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X#X##X#X#X#X#X#X#X#X
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PS Claim 3; Page 73-74; 90pp; Japanese.

XX
CC
The present sequence describes a method of controlling the secretion of corticotrophin releasing hormone (CRH), involving the use of a G protein receptor ligand. This can be used to control the secretion of CRH and is CC diseases an analgesic or for treating, preventing or amaliorating or disease (Including Doredom, nausea, pigmentation, hypogonadism, hair CC disease (Including Doredom, nausea, pigmentation, hypogonadism, hair CC loss, and hypotension), adrenal gland hypofunction and obesity. The CC loss, and hypotension), adrenal gland hypofunction of the CC present sequence is a peptide used in the exemplification of the CC invention.

XX
SQ Sequence 31 AA;

Query Match
Best Local Similarity 83.9%; Pred. No. 3.3e-17;
Bob ISKHKHSMERRTPDINPAWYXRGIRPVGRP 31

Search completed: December 3, 2003, 19:11:24
Job time: 33.75 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Tanaka, Yoko
APPLICANT: Mishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS: ADDRESS: DIKE, BROMSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER KEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,678A
FILING DATE: 26-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATORNEY/AGENT INFORMATION:
NAME: COALLIN, David G.
REGISTRATION NUMBER: 27,026
REGISTRATION NUMBER: 27,026
REGISTRATION NUMBER: 27,026
REGISTRATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAK: 617-523-3400
US-08-776-971-124
US-08-776-971-137
US-08-776-971-135
US-08-776-971-135
US-08-776-971-138
US-09-105-678A-7
US-09-105-678A-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 8, Application US/09105678A Patent No. 6103882 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 31 amino acids
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STATE: MA
COUNTY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
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Best Local Similarity
Matches 26; Conserv
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/BCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                                GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-176-971-47

US-08-776-971-61

US-08-471-208-8

US-09-421-208-9

US-09-421-208-9

US-09-421-208-37

US-09-421-208-43

US-09-560-915-14

US-09-956-915-14

US-09-956-915-15

US-09-956-915-15

US-09-956-915-15

US-09-956-916-15

US-09-105-6788-38

US-09-105-6788-38

US-09-105-6788-38

US-09-105-6788-44

US-08-776-971-62

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US-08-776-971-62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    328717 seqs, 42310858 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                         using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length
                                                                                                                                            - protein search,
                                                                                                                                                                                                                                                                                                                  Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                    Scoring table:
                                                                                                                                         OM protein
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| Sequence 43, Application US/09105678A
| Patent No. 6103882
| APPLICANT: Suenaga, Masato
| APPLICANT: Moriya, Takeo
| APPLICANT: Nathumra, Osamu
| TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
| TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
| STREET: 130 Water Street
| CITY: Boston
| STREET: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 31;
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                                                              COMPUTER READABLE FORM:

MEDIUM TYPE: Ploppy disk
MEDIUM TYPE: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COPERATION SYSTEM: PC-005/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,678A
FILING DATE: 26-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DAVING:
ATCHERYA ACKENT INFORMATION:
NAME: COLLIN, David G.,
REGISTRATION NUMBER: 27,026
RESTRENCE/DOCKET NUMBER: 27,026
RESTRENCE/DOCKET NUMBER: 48466-342
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF SEQ ID NO: 37:
BEQUENCE GIRRACTERISTICS:
INPORMATION FOR SEQ ID NO: 37:
BEGURANTE GIRRACTERISTICS:
LENGTH: 31 and no acids
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MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,678A
FILING DATE: 26-JUN-1998
PRIOR APPLICATION NUMBER: JP 172118/1997
PILING DATE: 37-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Conlin, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/POCKET NUMBER: 48466-342
TELECOMMUNICATION INFORMATION:
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Best Local Similarity 83.9%; Pred. No. 1.9e-17;
Matches 26; Conservative 0; Mismatches 5;
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STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
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US-09-105-678A-43
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Patent No. 6103882

GENERAL INFORMATION:

APPLICANT: Suenaga, Masato

APPLICANT: Tanaka, Yoko

APPLICANT: Tanaka, Yoko

TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND

NUMBER OF SEQUENCES: 52

CORRESPONDENCE ADDRESS:

ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP

STREET: 130 Water Street
                                                                                                                                         Sequence 9, Application US/09105678A

Fatent No. 6103882

GENERAL INFORMATION:
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Tanaka, Somu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,678A
FILING DATE: 26-JUN-1998
PRIOR APPLICATION NUMBER: UP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 SRXHXHSMEXRTPDINPAWYXXRGIRPVGRF 31
1 SRAHQHSMETRIPDINPAWYTGRGIRPVGRF 31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Conlin, David G.
REGISTRATION NUMBER: 27,026
REGISTRATION NUMBER: 48466-342
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERIFICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 130 Water Street CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 31 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 02109
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US-09-105-678A-37
                                                                                                     RESULT 2
US-09-105-678A-9
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Gaps
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HOBOYA, MABAKI
FUJII, RYO
FUJII, RYO
FULUMI, Shoji
KITAB OF INVENTION: POLYRROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Mater Street
CITY: BOSTON
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                            SOFTWARE: PastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 147; DB 3;
Pred. No. 1.9e-17;
0; Mismatches 5;
                                         CURRENT APPLICATION DATA:

APPLICATION NUBER: US/08/776,971B
FILING DATE: U6-Feb-1997
CLASSIFICATION NUBER: US/08/776,971B
PRIOR APPLICATION NUBER: PCT/JP96/03821
APPLICATION NUBER: PCT/JP96/03821
FILING DATE: 28-DEC-1996
APPLICATION NUBER: JP 7/34371
FILING DATE: 15-MAR-1996
APPLICATION NUBER: JP 8/211805
FILING DATE: 15-MAR-1996
APPLICATION NUBER: JP 8/246573
FILING DATE: 18-SEP-196
APPLICATION NUBER: JP 8/246573
FILING DATE: 18-SEP-196
APPLICATION NUBER: JP 8/246573
FILING DATE: 18-SEP-196
APPLICATION NUBER: J7,026
REGISTRATION NUBER: 27,026
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06-Feb-1997
CLASSIPICATION: <UNKnown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 SRXHXHSMEXRTPDINPAWYXXRGIRPVGRF 31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 47:
US-08-776-971-47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S-UB-//b->/1-D-
Sequence 61, Application US/08776971B
Patent No. 6228984
GENERAL INFORMATION:
APPLICANT: Hinuma, Shuji
Habata, Yugo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 31 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 617-523-6440
INPORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95.5%;
83.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26; Conservative
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Best Local Similarity
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Sequence 4, Application US/09172353
Patent No. 619530
APPLICANT: Stricker-Kongra, Alain
APPLICANT: GL, Wei
TITLE OF INVENTION: GPR.10 AS A TARGET FOR IDENTIFYING WEIGHT MODULATING COMPOUNDS
FILLE REPERENCE: 07334/102001
CURRENT APPLICATION NUMBER: US/09/172,353
CURRENT FILING DATE: 1998-10-14
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 4
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TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
                                                                                                                                                                                                                                                            95.5%; Score 147; DB 3; Length 31; 83.9%; Pred. No. 1.9e-17; ive 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 147; DB 3; Length 31;
Pred. No. 1.9e-17;
0; Mismatches 5; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kawamata, Yuji
Hosoya, Masaki
Fujii, Ryo
Fukusumi, Shoji
TELPRAX: 617-523-3400
TELPRAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 43: SEQUENCE CHARACTERISTICS: LENGTH: 31 amino acids TYPE: amino acids STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Hinuma, Shuji
Habata, Yugo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 02109
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 83.9°
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26; Conservative
                                                                                                                                                                         ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-105-678A-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Mus musculus
US-09-172-353-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Boston
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COUNTRY: USA
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Best Local Similarity
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US-08-776-971-47
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Tanaka, Yoko
APPLICANT: Mishimura, Osamu
IITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP STREET: 130 Water Street CITY: Boston STAIE: MA 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/421,208
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/105,678
FILING DATE: 26-JUN-1998
APPLICATION NUMBER: JP 172118/1997
ATTONING APPLICATION NUMBER: 37,026
REGISTRATION NUMBER: 27,026
REGISTRATION NUMBER: 27,026
REGISTRATION NUMBER: 27,026
REGISTRATION NUMBER: 37,026
TELERCOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 83.9%; Pred. No. 1.9e-17; Matches 26; Conservative 0; Mismatches 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 SRXHXHSMEXRIPDINPAWYXXRGIRPVGRF 31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 9, Application US/09421208 Patent No. 6258561
TELECOMMUNICATION INFORMATION:
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                              TELEPHONE: 617-523-3400
TELEPAK: 617-523-640
INPORMATION FOR SEQ ID NO: 8
SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
STRANDEDNESS
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                             ; MOLECULE TYPE: peptide US-09-421-208-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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02109
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Pred. No. 1.9e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5; Indels
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APPLICANT: Moriya, Takeo
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Tanaka, Yoko
APPLICANT: Mishimura, Osamu
IITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS: ADDRESS: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 02109
COMPUTER REDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CORPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/421,208
                          PADLICATION NUMBER: PCT/JP96/03821
PILING DATE: 28-DEC-1996
APPLICATION NUMBER: DF 7/34331
PILING DATE: 28-DEC-1996
APPLICATION NUMBER: JF 8/59419
PILING DATE: JF MAR-1996
APPLICATION NUMBER: JF 8/211805
PILING DATE: JF MAR-1996
APPLICATION NUMBER: JF 8/46573
PILING DATE: JF 8-EPF-1996
ATTORNEY AGENT INFORMATION:
NAME: CONLIN, DAVIG G.
REGISTRATION NUMBER: 27,026
REGISTRATION NUMBER: 27,026
REGISTRATION NUMBER: 27,026
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 SRTHRHSMEIRTPDINPAWYASRGIRPVGRF 31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
95.5%; Score 147; DE
Best Local Similarity 83.9%; Pred. No. 1.96
Matches 26; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HOLECULE TYPE: protein
HRACHENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 61:
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REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48466-342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/105,678
FILING DATE: 26-JUN-1998
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 8
US-09-421-208-8
Sequence 8, Application US/09421208
Patent No. 6258561
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 31 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
       PRIOR APPLICATION DATA:
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STATE: MA
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Sequence 14, Application US/09560915

Patent No. 6383764

GENERAL INFORMATION:

APPLICANT: Civelli, Oilvier

APPLICANT: Lin, Steven

TITLE OF INVENTION: Relating To Prolactin Releasing Peptide (PrRP)

FILE REPRENCE: P-UC 3334

CURRENT FILING DATE: 2000-04-28

NUMBER OF SEQ ID NOS: 24

SOFTWARE: PASTSEQ for Windows Version 4.0

SEQ ID NO 14

"LENGTH: 31

"WURDE NO. 14
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                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/421,208
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/105,678
FILING DATE: 26-JUN-1998
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
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REGISTRATION NUMBER: 27,026
REFRENCE/DOCKET NUMBER: 4846
TELECOMMUNICATION INPORMATION:
TELEPAK: 617-523-3400
TELEPAK: 617-523-3400
INPORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
    130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 31 amino acids
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Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: peptide US-09-421-208-43
                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
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                                                     . USA
02109
RF*
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US-09-560-915-14
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                                                                                                                        Sequence 37. Application US/09421208
Patent No. 625851
GENERAL INFORMATION:
APPLICANT: Suenaga, Masato
APPLICANT: Tanaka, Yoko
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: 130 Water Street
CITY: Boston
STRET: MA
COUNTY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 95.5%; Score 147; DB 3; Length 31; Best Local Similarity 83.9%; Pred. No. 1.9e-17; Matches 26; Conservative 0; Mismatches 5; Indels
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Patent No. 6258561
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Suemage, Masato
APPLICANT: Tanaka, Yoko
APPLICANT: Tanaka, Yoko
APPLICANT: Mishiura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/421,208 FILING DATE:
1 SRXHXHSMEXRTPDINPAWYXXRGIRPVGRF 31
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PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRILING DATE: 26-JUN-1998
PILING DATE: 27-JUN-1999
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY-AGENT INFORMATION:
NAME: CONLIN, David G.
REGISTRATION NUMBER: 27,026
REGISTRATION NUMBER: 48466-342
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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US-09-421-208-43
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Query Match 95.5%; Score 147; DB 3; Length 32; Best Local Similarity 83.9%; Pred. No. 2e-17; Matches 26; Conservative 0; Mismatches 5; Indels
                                                                                      COMPUTER READABLE FORM:

MEDIUM TYPE: Ploppy disk

COMPUTER: Ploppy disk

COMPUTER: Ploppy disk

COMPUTER: Ploppy disk

COMPUTER: PatentIn Release #1.0, Version #1.30

CURREATION SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURREATION NUMBER: US/09/105,678A

PILING DATE: 26-JUN-1998

PRILOR APPLICATION DATA:

APPLICATION NUMBER: US/09/105,678A

ATTORNEY/AGENT INFORMATION:

RESTRANCE/DOCKET NUMBER: 27,026

RESTRENCE/DOCKET NUMBER: 27
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MOLECULE TYPE: peptide
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                           COUNTRY: US
ZIP: 02109
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; Patent No. 6537765
; GENERAL INFORMATION:
APPLICANT: Gu, Wei
; APPLICANT: Gu, Wei
; TITLE OF INVENTION: GPRIO AS A TARGET FOR IDENTIFYING WEIGHT MODULATING COMPOUNDS
; FILLE REFERENCE: 07334/102001
; CURRENT APPLICATION NUMBER: US/09/799,955
; CURRENT PILING DATE: 2001-03-06
; PRIOR APPLICATION NUMBER: US/09/172,353
; PRIOR FILING DATE: 1998-10-14
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FREUSEQ FOR Windows Version 3.0
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           Sequence 15, Application US/09560915
Fatent No. 6383764
GENERAL INFORMATION:
APPLICANT: CIVElli, Olivier
APPLICANT: CIVElli, Olivier
TITLE OF INVENTION: Therapeutic Compositions and Methods
TITLE OF INVENTION: Relating To Prolactin Releasing Peptide (PrRP)
FILE REFERENCE: P-UC 3534
CURRENT APPLICATION NUMBER: US/09/560,915
CURRENT FILING DATE: 2000-04-28
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Fateseq for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 95.5%; Score 147; DB 4; Length 31; Best Local Similarity 83.9%; Pred. No. 1.9e-17; Matches 26; Conservative 0; Mismatches 5; Indels
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APPLICANT: Wenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Tanaka, Yoko
APPLICANT: Mishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             B: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
130 Water Street
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; LENGTH: 31
; TYPE: PRT
; ORGANISM: Wus musculus
US-09-799-955-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; LENGTH: 31
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-560-915-15
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US-09-105-678A-38
US-09-560-915-15
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US-09-799-955-4
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APPLICANT: Civelli, Olivier APPLICANT: Lin, Steven
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Sequence 15, Appl
Sequence 15, Appl
Sequence 4, Appli
Sequence 9, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 96, Appl
Sequence 96, Appl
Sequence 94, Appli
Sequence 94, Appli
Sequence 94, Appli
Sequence 94, Appli
Sequence 13, Appli
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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Sequence 39,
Sequence 40,
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'(gm2_6')ptodata'1/pubpaa/USO6_NEW PUB.pep:*
'(gm2_6')ptodata'1/pubpaa/USO6_NEW PUB.pep:*
'(gm2_6')ptodata'1/pubpaa/USO6_PUBCOMB.pep:*
'(gm2_6')ptodata'1/pubpaa/USO7_NEW PUB.pep:*
'(gm2_6')ptodata'1/pubpaa/PCTUG_NEW PUB.pep:*
'(gm2_6')ptodata'1/pubpaa/USO8_NEW PUB.pep:*
'(gm2_6')ptodata'1/pubpaa/USO8_PUBCOMB.pep:*
'(gm2_6')ptodata'1/pubpaa'USO8_PUBCOMB.pep:*
'(gm2_6')ptodata'1/pubpaa'USO8_PUBCOMB.pep:*
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'(gm2_6')ptodata'1/pubpaa'USO8_PUBCOMB.pep:*
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'(gm2_6')ptodata'1/pubpaa/USO8_PUBCOMB.pep:*
'(gm2_6')ptodata'1/pubpaa/USO8_PUBCOMB.pep:*
                           GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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154
1 SRXHXHSMEXRIPDINPAWYXXRGIRPVGRF 31
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US-09-932-161-15
US-10-096-777-114
US-10-044-592-8
US-10-044-592-9
US-10-044-592-9
US-10-044-592-96
US-10-044-592-96
US-10-044-592-94
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                     Title:
Perfect score:
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No.
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146   94   94   94   94   94   94   94	41, Appl 28, Appl 82, Appl 84, Appl 86, Appl 26, Appl 18, Appl 16, Appl 16, Appl 16, Appl 16, Appl 17, Appl 16, Appl 17, Appl 18, Appl 10, Ap		°
94.8 33 14 US-10-044-592-28 Sequence 94.8 98 14 US-10-044-592-28 Sequence 94.8 98 14 US-10-044-592-88 Sequence 94.8 98 14 US-10-044-592-89 Sequence 96.2 20 9 US-09-932-161-18 Sequence 67.5 20 9 US-09-932-161-16 Sequence 67.5 20 9 US-09-932-161-16 Sequence 67.5 20 12 US-10-064-777-18 Sequence 67.5 20 12 US-10-064-777-16 Sequence 67.5 20 12 US-10-064-777-16 Sequence 67.5 20 14 US-10-044-592-8 Sequence 67.5 20 14 US-10-044-592-9 Sequence 67.5 20 14 US-10-062-599-163 Sequence 67.5 20 14 U	1000140000 .00r .1m4r0 .0 .000000		3aps
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116 117 118 119 119 119 119 119 119 119 119 119		2-161-14 ice 14, Api No. US20i Lu INPORMA CANT: CIVI CANT: CIVI CANT: Li COF INVENT REFERENCE NT APPLICAT RO 14 RO 14 TH: 31 RISM: RALI RO 14 RESEAURA REFERENCE REFER	Match cocal Simi s 26; 1 SRX 1 SRX 2-161-15 2-161-15 Co- US, App No. US200 L INFORMA
RESERVE OF THE STATE OF THE STA	00000000000000000000000000000000000000	RESULT 1 US-09-93 Sequent Patent GENERA APPLI TITLE TITLE TITLE TITLE CURRE CURRE PRIOR PR	Query Best L Matche My Db Db RESULT 2 US-09-93 ; Sequent ; Patent

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i TYPE: PRTj ORGANISM: Homo SapienUS-10-096-777-15
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ORGANISM: Murine
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US-10-096-777-15
sequence 15, Application US/10096777
sequence 15, Application US/10096777
sequence 15, Division US/10011270A1
sequence 15, Application No. US20030171270A1
sequence 10. US20030171270A1
sequence 10. US20030171270A1
string of INVENTION: Therapeutic Compositions and Methods
string of INVENTION: Therapeutic Compositions and Methods
string REFERENCE: P-UC 3534
scurrent PILING DATE: 2002-03-12
sprior Application NUMBER: US/10/096,777
scurrent Filing DATE: 2000-04-28
sprior Application NUMBER: US/09/560,915
sprior SEQ ID NOS: 24
sscylb NO 15s
sequence 15,000-04-28
sprior SEQ ID NO 15
sequence 15,000-04-28
sprior MUMBER of SEQ for Windows Version 4.0
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| Sequence 14, Application US/10096777
| Sequence 14, Application US/10096777
| Publication No. 1020030171270A1
| GENERAL INFORMATION:
| APPLICANT: Civelli, Olivier
| APPLICANT: Lin, Steven
| TILLE OF INVENTION: Therapeutic Compositions and Methods
| TILLE OF INVENTION: Relating To Prolactin Releasing Peptide (PRRP)
| TILLE OF INVENTION: Relating To Prolactin Releasing Peptide (PRRP)
| TILLE OF INVENTION: Relating To Prolactin Releasing Peptide (PRRP)
| TILLE OF INVENTION: 2002-03-12
| FILLE REFERENTE: 2002-03-12
| PRIOR PAPLICATION NUMBER: US/09/560,915
| PRIOR FILING DATE: 2000-04-28
| NUMBER OF SEQ ID NOS: 24
| SEQ ID NOS: 24
| SEQ ID NOS: 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 95.5%; Score 147; DB 9; Length 31; Best Local Similarity 83.9%; Pred. No. 6.8e-16; Matches 26; Conservative 0; Mismatches 5; Indels
TITLE OF INVENTION: Screening and Therapeutic Methods For TITLE OF INVENTION: Promoting Wakefulness and Sleep FILE REPERENCE: P-UC 4679 CURRENT APPLICATION NUMBER: US/09/932,161 CURRENT FILING DATE: 2001-08-17 PRIOR APPLICATION NUMBER: US 09/560,915 PRIOR APPLICATION NUMBER: US 09/560,915 PRIOR PILING DATE: 2000-04-28 NUMBER OF SEQ ID NOS: 24 SOFTWARE PARESEQ for Windows Version 4.0 SEQ ID NO 15 LENGTH: 31
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Best Local Similarity 83.99
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Homo Sapien
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US-10-044-592-96

Sequence 96, Application US/10044592

Publication No. US20020143152A1

GENERAL INFORMATION:

APPLICANT: Hinuma, Shuji

TITLE OF INVENTION: Polypeptides, their Production and Use

FILE REFERENCE: 2463US2P

CURRENT FILING DATE: 2002-01-10

FRIOR PAPLICATION NUMBER: US/10/044,592

PRIOR PLING DATE: 1999-25-10

PRIOR PLING DATE: 1999-25-10

PRIOR APPLICATION NUMBER: PCT/JP98/01923

PRIOR APPLICATION NUMBER: PCT/JP98/01923

PRIOR APPLICATION NUMBER: JP 9-109974

PRIOR PILING DATE: 1997-04-28

SOFTWARE:

SEQ ID NO 96

LENGTH: 86

"LENGTH: 86

"TO THE OF SEQ ID NOS: 96

"LENGTH: 86
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Sequence 92, Application US/10044592

Publication No. US20020143152A1

GENERAL INFORMATION:

APPLICANT: Hunma, Shujj

APPLICANT: Fukusumi, Shoji

ITILB OF INVENTION: Polypeptides, their Production and Use

FILE REFERNCE: 2463U52P

CURRENT APPLICATION NUMBER: US/10/044,592

CURRENT FILING DATE: 2002-01-10

PRIOR PILING DATE: 1998-04-27

PRIOR FILING DATE: 1998-04-27

PRIOR FILING DATE: 1998-04-27

PRIOR FILING DATE: 1997-04-28

NUMBER OF SKQ ID NOS: 96
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; LCCATION: (1224)..(1243)
; OTHER INFORMATION: Bracket region depicted in FIG 39.
US-10-044-592-96
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Pred. No. 1.9e-15;
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95.5%; Score 147; DB 14;
Best Local Similarity 83.9%; Pred. No. 1.9e-15;
Matches 26; Conservative 0; Mismatches 5;
                                                                       21 SRAHQHSMETRTPDINPAWYTGRGIRPVGRF 51
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       Mismatches
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Best Local Similarity 83.9
Marches 26; Conservative
    26; Conservative
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US-10-044-592-92
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LENGTH: 87
TYPE: PRT
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Publication No. US20020143152A1;
GENERAL INPORMATION:
APPLICANT: Hinuma, Shuji
TITLE OF INVENTION: Polypeptides, their Production and Use
FILE REFERENCE: 2463U52P
CURRENT APPLICATION NUMBER: US/10/044,592
CURRENT FILING DATE: 2002-01-10;
FRIOR APPLICATION NUMBER: US/99403639
PRIOR PILING DATE: 1999-25-10
PRIOR APPLICATION NUMBER: PCT/JP98/01923;
PRIOR APPLICATION NUMBER: PCT/JP98/01923;
PRIOR APPLICATION NUMBER: PCT/JP98/01923;
PRIOR APPLICATION NUMBER: US/90-6-27;
PRIOR PILING DATE: 1999-04-27;
PRIOR PILING DATE: 1997-04-28
                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Hinum, Shuji
APPLICANT: Hinum, Shuji
APPLICANT: Hinum, Shoji
TITLE OF EKUSUMION: Polypeptides, their Production and Use
FILE REPERENCE: 2453U32P
CURRENT APPLICATION NUMBER: US/10/044,592
CURRENT APPLICATION NUMBER: US/10/044,592
CURRENT FILING DATE: 1999-25-10
PRIOR FILING DATE: 1999-25-10
PRIOR FILING DATE: 1999-04-27
PRIOR FILING DATE: 1999-04-27
PRIOR FILING DATE: 1999-04-27
PRIOR FILING DATE: 1997-04-28
NUMBER OF SEQ ID NOS: 96
                                                                  Query Match 95.5%; Score 147; DB 14; Length 31; Best Local Similarity 83.9%; Pred. No. 6.8e-16; Matches 26; Conservative 0; Mismatches 5; Indels
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Pred. No. 1.6e-15;
0; Mismatches 5; Indels
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Pred. No. 1.8e-15;
                                                                                                                                                               1 SRXHXHSMEXRIPDINPAWYXXRGIRPVGRF 31
                                                                                                                                                                                             1 SRAHQHSMETRIPDINPAWYTGRGIRPVGRF 31
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                                                                                                                                                                                                                                                                                               US-10-044-592-90

'Sequence 90, Application US/10044592

'Publication No. US20020143152A1

'GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95.5%;
83.9%;
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Best Local Similarity 83.9%;
Matches 26; Conservative (
; OTHER INFORMATION: antigen US-10-044-592-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , ORGANISM: Rat
US-10-044-592-90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-044-592-1
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LENGTH: 70
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LENGTH: 82
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US-10-096-777-13

| Sequence 13, Application US/10096777
| Publication No. US20030171270A1
| GENERAL INFORMATION:
| APPLICANT: Civelli, Olivier
| APPLICANT: Lin, Steven
| TITLE OF INVENTION: Therapeutic Compositions and Methods
| TITLE OF INVENTION: Relating To Prolactin Releasing Peptide (PFRP)
| TITLE OF INVENTION: 2003-03-12
| FILE REFERENCE: P-UC 3534
| CURRENT PELLING DATE: 2002-03-12
| PRIOR APPLICATION UNMERR: US/10/096,777
| TRINGO DATE: 2002-03-12
| PRIOR FILING DATE: 2000-04-28
                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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APPLICANT: Fukusumi, Shuji
FILE REPERENCE: 2463US2P
FILE REPERENCE: 2463US2P
CURRENT APPLICATION NUMBER: US/10/044,592
CURRENT APPLICATION NUMBER: US/39403639
PRIOR PILING DATE: 1999-25-10
PRIOR PILING DATE: 1999-25-10
PRIOR PLING DATE: 1999-4-27
PRIOR FILING DATE: 1999-64-27
PRIOR FILING DATE: 1997-64-28
NUMBER OF SEQ ID NOS: 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94.8%; Score 146; DB 14; Length 31;
83.9%; Pred. No. 9.7e-16;
ive 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 94.8%; Score 146; DB 12; Length 31; Best Local Similarity 83.9%; Pred. No. 9.7e-16; Matches 26; Conservative 0; Mismatches 5; Indels
                          5; Indels
83.9%; Pred. No. 9.7e-16;
tive 0; Mismatches 5
                                                                                                            1 SKAHQHSMEIRTPDINPAWYAGRGIRPVGRF 31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 24
SOFTWARR: FastSEQ for Windows Version 4.0
SEQ ID NO 13
LENGTH: 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 39, Application US/10044592
Publication No. US20020143152A1
GENERAL INPORMATION:
                        26, Conservative
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Best Local Similarity 83.9
Matches 26; Conservative
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: BOB taurus
US-10-096-777-13
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LENGTH: 31
                        Matchee
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COTHER INFORMATION: primer
NAME/KEY: misc_feature
LOCATION: (925)..(955)
COTHER INFORMATION: primer
NAME/KEY: misc_feature
LOCATION: (1)...(955)
COTHER INFORMATION: insert fragment of pmGB3 as depicted in PIG 36 and 37.US-10-044-592-94
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                                                                                                                                                                                                                                                APPLICANT: Hinum, Shuji
APPLICANT: Fukusumi, Shuji
APPLICANT: Fukusumi, Shoji
TITLE OF INVENTION Polypeptides, their Production and Use
FILE REPERENCE: 246:3082P
CURRENT APPLICATION NUMBER: US/10/044,592
CURRENT APPLICATION NUMBER: US 09/403639
PRIOR APPLICATION NUMBER: US 09/403639
PRIOR FILING DATE: 1999-25-10
PRIOR FILING DATE: 1998-04-27
PRIOR FILING DATE: 1998-04-27
PRIOR FILING DATE: 1997-04-28
NUMBER OF SEQ ID NOS: 96
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Patent No. US2002037533A1

GENERAL INFORMATION:

APPLICANT: Civelli, Olivier

APPLICANT: Lin, Steven

TITLE OF INVENTYON: Screening and Therapeutic Methods For TITLE OF INVENTYON: Screening Wakefulness and Sleep

FILE REFERENCE: Promoting Wakefulness and Sleep

CURRENT APPLICATION NUMBER: US/09/932,161

CURRENT FILING DATE: 2001-08-17

PRIOR APPLICATION NUMBER: US 09/560,915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94.8%; Score 146; DB 9; Length 31;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 147; DB 14
Pred. No. 2e-15;
                                                    23 SRTHRHSMBIRTPDINPAWYASRGIRPVGRF 53
                        1 SRXHXHSMEXRIPDINPAWYXXRGIRPVGRF 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 SRXHXHSMEXRTPDINPAWYXXRGIRPVGRF 31
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13
LENGTH: 31
                                                                                                                                                                                    Sequence 94, Application US/10044592
Publication No. US20020143152A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 83.9%;
Matches 26; Conservative
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NAME/KEY: misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 12
US-09-932-161-13
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LENGTH: 91
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RESULT 15
US-10-044-592-40
is Sequence 40, Application US/10044592
is Dublication No. US20020143152A1
is GEREAL INFORMATION:
is APPLICANT: Hinuma, Shuji
is APPLICANT: Hinuma, Shuji
is TITLE OF INVENTION: Polypeptides, their Production and Use FILE REFERENCE: 2463US2P
is CURRENT APPLICATION NUMBER: US/10/044,592
current PILING DATE: 2002-01-10
prior APPLICATION NUMBER: US 09/403639
prior FILING DATE: 1999-25-10
ip PRIOR PILING DATE: 1999-04-27
prior APPLICATION NUMBER: PCT/JP98/01923
ip PRIOR PILING DATE: 1997-04-28
is PRIOR PILING DATE: 1997-04-28
is DRIOR PILING DATE: 1997-04-28
is SOFTWARE:
is SEQ ID NO 40
it LENGTH: 32
it TYPE: PRI
is ORGANISM: Bovine
US-10-044-592-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 94.8%; Score 146; DB 14; Length 32; Best Local Similarity 83.9%; Pred. No. 1e-15; Matches 26; Conservative 0; Mismatches 5; Indels
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Gaps ö

> 1 SRXHXHSMEXRTPDINPAWYXXRGIRPVGRF 31

ò g Search completed: December 3, 2003, 19:17:38 Job time : 23.5 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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protein search, using sw model • OM protein December 3, Run on:

2003, 19:05:30 ; Search time 10.5 Seconds (without alignments) 283.927 Million cell updates/sec

pol polyprotein ARP1 protein - yea
pol polyprotein HIV-1 retropepsin
HIV-1 retropepsin
hypothetical prote
hypothetical prote

ALIGNMENTS

RESULT 1

probable 1,2-dloxy opsin, ocellar - A opsin, lateral eye probable and prot probable anino aci probable inner mem inner membrane tra

P91007 H85851 B48197 B48197 D70885 G64720 G85480 G85480 A42743 S61046 GNMVGV GNMVGV GNMVGV T16859

probable gentisate

Title: Perfect score:

US-09-868-885B-44 154 1 SRXHXHSMEXRIPDINPAWYXXRGIRPVGRF 31 Sequence:

Scoring table:

283308 seqs, 96168682 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 76:*
1: pirl:*
2: pir2:*
3: pir3:*
4: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

conserved hypothet probable glutathic hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote probable unr prote my probable magnesium ferripyochelical prote probable magnesium ferripyochelical prote probable 1-acylgly hypothetical prote probable 1-acylgly hypothetical prote probable regulator ubiquinone biosynt hypothetical prote prolactin-releasin Description JC7607 P83376 P83376 P83376 P76959 P76959 P76969 P750904 P750904 P750904 P750904 P750904 P750904 P750904 P750904 P750904 P760904 P7609 DB Query Match Length Score Result No. 

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Length 664;

DB 2;

Score 49.5;

32.1%;

Query Match

4

62.5%; Pred. No. 8.1; tive 1; Mismatches

Best Local Similarity 62.5 Matches 10; Conservative

478 TPDINP-WFLQRSGRP 492

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27

12 TPDINPAWYXXRGIRP

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hypothetical protein Atu5077 [imported] - Agrobacterium tumefaciens (strain C58, Dupont C; Species: Agrobacterium tumefaciens
C; Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
C; Accession: A2169
R; Mood, DW,; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClel Rarp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A; Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, eter, B.W.
A; Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A; Rocession: AC3169
A; Accession: AC316
A; Accession: AC316
A; Mosidues: 1-118 < KUR>
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C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Spacesion: B70569
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, C, Conarcher, R.; Davies, R.; Devlini, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, E, Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
Nature 393, 537-544, 1998
A;Authors: Squares, R.; Sulston, J.B.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Authors: Squares, R.; Sulston, J.B.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Reference number: A70500; MUID: 98295987; PMID: 9634230
A;Reference number: A70569
A;Accesslan: B70569
A;Accesslan: B70569
A;Actus: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                       A;Accession: 876955
A;Status: preliminary
A;Molecule type: DNA
A;Rediques: 1-128 «CAN»
A;Ccoss-references: EMBL:D90917; GB:AB001339; NID:g1653836; PIDN:BAA18867.1; PID:d10196
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
                                    Cjaccession: 876955
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, B.; Nakamura, Y.; Miyajima, N. O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuc DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocysti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ä
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A,Experimental source: strain C58 (Dupont)
CiDate: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 30.5%; Score 47; DB 2; Length 128; Best Local Similarity 33.3%; Pred. No. 3.8; Matches 11; Conservative 5; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Length 118;
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                                                                                                                                                                                                                                                      A; Reference number: S74322; MUID: 97061201; PMID: 8905231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11 SPENNOSLDCSSPDPSRKWYQARLFSFGITPTG 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 SRXHXHSMEXRTPDINPAWYXXR----GIRPVG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19 KLHKHNAARRRPDIGARVOPATAPHRGLAGIG 50
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Local Similarity 34.4%;
les 11; Conservative 4
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Matches
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                                                                                                                                                                                                                                                                                                                                              probable glutathione S-transferase PA2821 [imported] - Pseudomonas aeruginosa (strain PA C;Species: Pseudomonas aeruginosa (c;Species: Pseudomonas aeruginosa (strain PA C;Species: Pseudomonas (strain PA C;Species: Pseudomonas (strain PA C;Species: Pseudomonas aeruginosa PA01, an opportunistic pathota;Species: Pseudomonas aeruginosa PA01, an opportunistic pathota;Paccession: C33292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein P15G16.60 - Arabidopsis thaliana (5/species: Arabidopsis thaliana (mouse-ear cress) (5/species: Arabidopsis thaliana (mouse-ear cress) (5/species: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000 (5/sccession: T47959 (7/sccession: T47959 (7/sccession: T47959 (7/sccession: T47959 (7/screen) Squence Database, January 2000 (7/sccession: T47959 (7/screen) A/sccession: T47959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Residues: 1-220 <STO>
A;Cross-references: GB:AE004709; GB:AE004091; NID:g9948904; PIDN:AAG06209.1; GSPDB:GN001
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Pred. No. 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
31.8%; Score 49; DB 2; Length 220;
Best Local Similarity 44.0%; Pred. No. 3.1;
Matches 11; Conservative 3; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7; Indels
                                               Indels
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hypothetical protein - Synechocystis sp. (strain PCC 6803)
C;Species: Synechocystis sp.
A;Variety: PCC 6803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Experimental source: cultivar Columbia; BAC clone F15G16
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A, Experimental source: strain PAO1 C, Genetics: G, Gene: PA2821 C, Superfamily: plaice glutathione transferase

Status: preliminary Molecule type: DNA

6 HSMEXRTPDINPAWYXXRGIRPVGR 30 

ઠે 셤 3; Mismatches

Query Match
Best Local Similarity 47.4%;
Matches 9; Conservative

A;Map position: 3 A;Introns: 39/1; 678/2; 698/3; 773/2 A;Note: F15G16.60

Genetics:

A,Molecule type: DNA A,Residues: 1-790 <DEH> A,Cross-references: EMBL:AL132959

A;Status: preliminary A;Molecule type: DNA

366 PPHNPRTYGSRGLOPHGRW 384

RESULT 5

13 PDINPAWYXXRGIRPVGRF 31

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112 RKRLHQLELAQPDLNEGW 129
                                                                                                                                                                                                                                                                                                                          2 RXHXHSMEXRTPDINPAW 19
                                                                                                                                                                                                               Query Match 29.9%;
Best Local Similarity 38.9%;
Matches 7; Conservative
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Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      probable unr protein - rat
A, Residues: 1-348 <WIL>
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Best Local S:
Matches 9
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T31462
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A; Residues: 1-333 <SIM>
A; Residues: 1-333 <SIM>
A; Cross-references: GB:ABC03860; GB:ABC03849; NID:g9104830; PIDN:AAF82881.1; GSPDB:GN001
A; Experimental source: strain 9a5c
B; Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Carraro, D.M.; Carrer, H. Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H. Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Franca, S.C.; Franco, D.M.; Carrer, H. Briones, M.R.S.; Bueno, M.R.P.; Kitajima, J.S.; Franca, S.C.; Franco, M.C.; Frohm J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kiramae, E.B.; Laigu Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E.G.; Ninses, E.C.; Miramae, E.C.; Martins, A.A. Maciara, A.M.B.N.; Macleira, M.C.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.R. A; Authors: da Silva, A.C.R.; da Silva, M.M.; Silva Jr., W.A.; de Silva, M.B.; Silva Jr., W.A.; de Silva, M.B.; Silva Jr., W.A.; de Silva, A.M.; Silva Jr., W.A.; de Silva, F.R.; Sawasak A; Conteins: annotation
A; Conteins: annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hydroxybenzoate octaprenyltransferase XF0068 [imported] - Xylella fastidiosa (strain 9a5
C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 17-Nov-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Accession: H82852
R; anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen Rstanonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen Asture 406, 151-157, 2000
A; Title: 406, 151-157, 2000
A; Reference number: A82515; MUID: 20365717; PMID: 10910347
A; Reference number: A82515; MUID: 20365717; PMID: 10910347
                A;Cross-references: GB:Z95390; GB:AL123456; NID:g3261766; PIDN:CAB08708.1; PID:g2104408
A;Experimental source: strain H37Rv
                                                                                                     A,Gene: Rv2485c
C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
F;46-227/Domain: short-chain alcohol dehydrogenase homology <SADH>
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T21648
T21648
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: T21648
R;Basham, V.
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                                                                                                                                                                                                                     Length 314;
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C;Superfamily: 4-hydroxybenzoate octaprenyltransferase
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submitted to the EMBL Data Library, October 1996
A;Reference number: 219453
A;Accession: T21648
A;Scatus: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                               Score 46; DB 2;
Pred. No. 14;
4; Mismatches 11
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Pred. No. 15;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                               205 HWMKLAADELGPSWVRVNSIRP 226
                                                                                                                                                                                                                                                                                                                                6 HSMEXRTPDINPAWYXXRGIRP 27
                                                                                                                                                                                                               Query Match
Best Local Similarity 31.8%;
Matches 7; Conservative 4
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ilarity 53.3%;
Conservative
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Best Local Similarity
  A; Residues: 1-314 <COL>
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A, Status: preliminary
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T50904
Mg protoporphyrin methyl transferase [imported] - Rubrivivax gelatinosus
C;Species: Rubrivivax gelatinosus
C;Species: Rubrivivax gelatinosus
C;Species: 21-Jul-1000 #sequence_revision 21-Jul-2000 #text_change 02-Sep-2000
C;Accession: T50904
C;Accession: T50904
SiNagashima, K.V.; Igarashi, N.; Harada, J.; Nagashima, S.; Matsuura, K.; Shimada, K.
Bubmitted to the EMBL Data Library, November 1999
A;Description: Determination of Nucleotide Sequences of Rubrivivax gelatinosus Photosyn
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C,Superfamily: Rhodobacter capsulatus magnesium-protoporphyrin O-methyltransferase
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A;Cross-references: EMBL:281074; PIDN:CAB03039.1; GSPDB:GN00022; CESP:F32B6.3 A;Experimental source: clone F32B6 (jGenetics: Cigenetics: A;Gene: CESP:F32B6.3 A;Gene: CESP:F32B6.3 A;Map position: 4 A;Introns: 56/3; 105/1; 146/3; 185/1; 223/1; 258/2; 320/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Rattus norvegicus (Norway rat)
C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 05-Nov-1999
C;Accession: S11210
R;Jcffers, M.; Paciucat, R.; Pellicer, A.
Nucleif Acids Res. 18, 4891-4899, 1990
A;Title: Characterization of unr; a gene closely linked to N-ras.
A;Reference number: S11210; MUID:90370473; PMID:2204029
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A,Residues: 1-798 <JRP>
A,Cross-references: EMBL:X52311; NID:g57454; PIDN:CAA36549.1; PID:g57455
C;Keywords: DNA binding
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                                                                                                                                                                                                                      Score 46; DB 2; Length 348;
Pred. No. 15;
2; Mismatches 9; Indels
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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A;Cross-references: EMBL:AB034704; PIDN:BAA94057.1
A;Experimental source: strain IL144
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A, Experimental source: cultivar Columbia; BAC clone F15A17
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Best Local Si
Matches 11;
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                                                            C,Genetics:
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D87559
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C;Species: Deinococcus radiodurans
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
C;Accession: B75318
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ms.; Shen, H.O.; Venter, J.C.; Fraser, C.M.
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probable magnesium chelatase (EC 4.99.1.-) chain H BchH - Heliobacillus mobilis C; Species: Heliobacillus mobilis C; Species: Heliobacillus mobilis C; Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 15-Sep-2000 C; Accession: T31462 R; Xiong, J.; Inoue, K.; Bauer, C.B. R; Xiong, J.; Inoue, K.; Bauer, C.B. Proc. Natl. Acad. Sci. U.S.A. 95, 14851-14856, 1998 A; Title: Tracking molecular evolution of photosynthesis by characterization of a major A; Accession: T31462 A; MUD:99061957; PMID:9843979 A; Accession: T31462 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       T48336

hypothetical protein F15A17.180 - Arabidopsis thaliana

hypothetical protein F15A17.180 - Arabidopsis thaliana

(Species: Arabidopsis thaliana (mouse-ear cress)

(Spate: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000

(SAccession: T48336

RiBevan, M.; Terryn, N.; Ardiles, W.; Buysshaert, C.; Dasseville, R.; De Clerck, R.; Sewes, H.W.; Rudd, S.; Lemcke, K.; Mayer, K.F.X.

submitted to the Protein Sequence Database, April 2000

A;Recence number: Z24491

A;Accession: T48336

A;Status: preliminary

A;Residues: 1-501 < ABEV>

A;Cross-references: EMBL:AL163002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Gene: bchH
C,Superfamily: Rhodobacter capsulatus magnesium-protoporphyrin O-methyltransferase
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A,Residues: 1-1292 <XIO>
A,Cross-references: EMBL:AF080002; NID:g3820536; PID:g3820560; PIDN:AAC84033.1
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63 HTLEDLTPDIHPTAFVAPSADVIGQ 87
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Best Local Similarity 32.0
Matches 8; Conservative
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C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001
C;Date: 20-Apr-2001
C;Accession: 101559
C;Accession: 107559
C;Accession: 107559
R;Accession: 107559
R;Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sensory box histidine kinase/response regulator [imported] - Caulobacter crescentus
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A;Residues: 1-637 <STO>
A;Cross-references: GB:AE005673; NID:g13424056; PIDN:AAK24472.1; GSPDB:GN00148
C;Genetics:
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                                                                                                                                                                                                                   Length 501
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                                                                                                                                                                                                        Score 45; DB 2;
Pred. No. 32;
4; Mismatches
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42.9%;
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                                                                                                                                                                 Query Match
Best Local Similarity 42.5.
Best Local 6; Conservative
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A, Map position: 5
A; Introns: 63/1; 194/2; 280/1
A; Note: F15A17.180
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (ISOFORM 2).
STRAIN=Spreague-Dawley; TISSUE=Hypothalamus;
Anderson S.T., Kokay I.C., Lang T., Grattan D.R., Curlewis J.D.;
"Quantitation of prolactin-releasing peptide (PrRP) mRNA expression in specific brain regions during the rat oestrous cycle and in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus (Rat).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalla, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                     TISSUB-Brain;
MEDLINE-986818; PubMed=9607765;
MEDLINE-986818; PubMed=9607765;
MINUME S., Habata Y., Fujii R., Kawamata Y., Hosoya M., Fukusumi S.,
Kitada C., Masuo Y., Asuo T., Matsumoto H., Sekiguchi M.,
Kurokawa T., Nishimura O., Onda H., Fujino M.;
"A prolactin-releasing peptide in the brain.";
                                                                                                                                                                         PRRP RAT

AC P81278; 08740.

AC P81278; 0883Y0;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 41, Last sequence update)

DT 28-PRB-2003 (Rel. 41, Last annotation update)

DR Prolactin-releasing peptide precursor (PrRP) (Prolactin-releasing bb hormone) [Contains: Prolactin-releasing peptide precursor (PrRP) (Prolactin-releasing bb hormone) [Contains: Prolactin-releasing peptide PrRP31; Prolactin-

DR releasing peptide PrRP20].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IsoId=P81278-2; Sequence=VSP 004370;
TISSUE SPECIFICITY: Widely expressed, with highest levels in
medulla oblongata and hypothalamus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    lactation.";
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IsoId=P81278-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORM 1).
TISSUE SPECIFICITY.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=1;
 RESULT 1
 rattus norv
homo sapien
bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                bos taurus
helicobacte
pasteurella
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                                                                December 3, 2003, 19:01:34; Search time 6.25 Seconds (without alignments) 233.252 Million cell updates/sec
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P32770
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P00306
P03943
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097859
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P08040
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Q92935
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          5.1.6
Compugen Ltd.
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                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                            127863 seqs, 47026705 residues
                                                                                                                                                                                                                                                                                                                                                 SUMMARIES
          GenCore version
Copyright (c) 1993 - 2003
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CYGR_ARBPU
ARGC_BACHD
Y468_MYCPN
LAR_CABEL
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PHAI FREDI
PHAI PSEA9
PHA2 FREDI
PHCA CYACA
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Y587 PASMU
NER3 HUMAN
UVRA METTH
OPS1 LIMPO
OPS2 LIMPO
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PRRP HUMAN
PRRP BOVIN
EXL1 HUMAN
UNR RAT
NER3 BOVIN
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CYCR_CHRVI
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PHCA_SYNY3
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                                                protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Match Length DB
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772
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corynebacte
escherichia
canis famil
corynebacte
escherichia
mus musculu
homo sapien
vibrio chol
rhizobium 1
rhizobium 1
 methanococc
                                                         Q8caq8 1
075534 1
Q9kuw5 1
Q98m36 1
P56899 1
         QBnrm3
P14375
P25473
Q8fqp1
P29013
057996
                                                                                                                                ALIGNMENTS
                  ZRAR_BCOLI
CLUS_CANFA
BX7L_COREF
YCGB_ECOLI
IMMT_MOUSE
UNR_HUMAN
                                                                              UVRA VIBCH
UVRA RHILO
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Сарв

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entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hinuma S., Habata Y., Pujii R., Kawamata Y., Hosoya M., Pukusumi S., Kitada C., Masuo Y., Asano T., Matsumoto H., Sekiguchi M., Kurokawa T., Wishimurao O., Onda H., Fujino M.;
Rurokawa T., Wishimurao O., Onda H., Fujino M.;
"A prolactin-releasing peptide in the brain.";
Nature 393:272-276(1998)
-!- FUNCTION: Stimulates prolactin (PRL) release and regulates the expression of prolactin through its receptor GPRIO. May stimulate lactotrophs directly to secrete PRL.
-!- TISSUE SPECIFICITY: MEDULIA OBLONGATA AND HYPOTHALAMUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
                                                                                                                                                                                                                                                                        AMIDATION (G-54 PROVIDE AMIDE GROUP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2003 (Rel. 41, Last annotation update)
Prolactin-releasing peptide precursor (PrRP) (Prolactin-releasing hormone) [Contains: Prolactin-releasing peptide PrRP31; Prolactin-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AMIDATION (G-54 PROVIDE AMIDE GROUP)
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PROLACTIN-RELEASING PEPTIDE PRRP20.
                                                                                                                                                                                             PROLACTIN-RELEASING PEPTIDE PRRP31.
PROLACTIN-RELEASING PEPTIDE PRRP20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AB015417; BAA29025.1; -.
Hormone; Amidation; Signal; Cleavage on pair of basic residues.
SIGNAL 1 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 98;
                                                                                                                                                                                                                                                                                                                                             Length 87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 146; DB 1; Length >> Pred, No. 1.2e-16;
                                                                                                                                                                                                                                                                                                                                             Score 147; DB 1; Length 87
Pred. No. 7.1e-17;
0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08AC35A13B0FA908 CRC64;
                                                                                                                                                                                                                                                                                            229A2F3F50CF981B CRC64;
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                                                                                                                                                                      BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                               1 SRXHXHSMEXRTPDINPAWYXXRGIRPVGRF 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A., AND SEQUENCE OF 23-52.
TISSUE-Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23 SRTHRHSMEIRTPDINPAWYASRGIRPVGRF
                                                                                              MIM; 602663; -.
GO; GO:0005180; F:peptide hormone; TAS.
Hormone; Amidation; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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98
53 A
10544 MW;
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llarity 83.9%;
Conservative
                                                                                                                                                                                                                                                                                                                                                95.5%;
83.9%;
                                                                          EMBL; AB015419; BAA29027.1;
                                                                                                                                                                                                                                                                                               9639 MW;
                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 83.9
nes 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               releasing peptide PrRP20]
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Best Local Similarity
26; Conserve
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                                                                                                                                                                                                                                                                                               87 AA;
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SEQUENCE
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PRRP BOVIN
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  use by non-profit institutions as long as its content is in no way additied and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                       AMIDATION (G-53 PROVIDE AMIDE GROUP).
IPDINPAWYTGRGIRPVGRFGRRRATPRDVTGLGQLSCLPL
                                                                                                                                                                                                                                                                                                                                                                                                DGRTKFSQRG -> SECLTYGKQPLTSFHPFTSQMPP (in
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-!- FUNCTION: Stimulates prolactin (PRL) release and regulates the expression of prolactin through its receptor GPR10. May stimulate lactotrophs directly to secrete PRL.
-!- TISSUE SPECIFICITY: MEDULLA OBLONGATA AND HYPOTHALAMUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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MEDLINE=9945652; PubMed=10498338;
Pujii R., Fukusumi S., Hosoya M., Kawamata Y., Habata Y., Hinuma S.,
Sekiguchi M., Kitada C., Kurokawa T., Nishimura O., Onda H.,
Sumino Y., Fujino M.;
                                              entitic.

or send an email to

R EMBL; AB015418; BAA29026.1; -.

R EMBL; AP521930; AAM82154.1; -.

R EMBL; AP521930; AAM82154.1; -.

R Hormone; Amidation; Signal; Cleavage on pair of basic residues; KW Alternative splicing.

FT SIGNAL 1 21 BY SIMILARITY.

FT PEPTIDE 22 52 PROLACTIN-RELEASING PEPTIDE PRRP31.

FT PROPEP 57 83 AMIDATION (G-53 PROVIDE AMIDE GROUP)

FT PROPEP 57 83 AMIDATION (G-53 PROVIDE AMIDE GROUP)

FT PROPEP 57 83 AMIDATION (G-53 PROVIDE AMIDE GROUP)

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FT PROPEP 57 83 AMIDATION (G-53 PROVIDE AMIDE GROUP)
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30-MAY-2000 (Rel. 39, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Prolactin-releasing peptide precursor (PrRP) (Prolactin-releasing
hormone) (Contains: Prolactin-releasing peptide PrRP31; Prolactin-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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MEDLINE-98268781; PubMed=9607765;

Hinuma S., Habatea Y., Fujii R., Kawamata Y., Hosoya M., Fuj

Kitada C., Masuo Y., Asano T., Matsumoto H., Sekiguchi M.,

Kitada T., Nishimura O., Onda H., Fujino M.;

"A prolactin-releasing peptide in the brain.";

Nature 393:272-276(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 147; DB 1; Length 83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOC75A264EEE4F29 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6.8e-17;
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83.9%;
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P81277;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE=97189339; PubMed=9037597;
Wise C.A., Clines G.A., Massa H., Trask B.J., Lovett M.;
"Identification and localization of the gene for EXTL, a third member of the multiple exostoses gene family.";
Genome Res. 7:10-16(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A., AND VARIANT HIS-379.
MEDLINE=99408231; PubMed=10480354;
Xu L., Xia U., Jiang H., Zhou J., Li H., Wang D., Pan Q., Long Z., Fan C., Deng H.-X.;
"Mutation analysis of hereditary multiple exostoses in the Chinese.";
Hum. Genet. 105:45-50(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wuyts W., Spieker N., Van Roy N., De Paepe A., De Boulle K.,
Willems P.J., Van Hul W., Versteeg R., Speleman F.;
"Refined physical mapping and genomic structure of the EXTL1 gene.";
Submitted (MAY.1999) to the RMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: UDP-N-acetyl.-D-glucosaminyl-proteoglycan =
UDP + N-acetyl-alpha-D-glucosaminyl-proteoglycan =
UDP + N-acetyl-alpha-D-glucosaminyl-proteoglycan.
-!- SUBCELLUAR LOCATION: Type II membrane protein. Bndoplasmic
reticulum (By similarity).
-!- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 47.
                                                                                                                                                                                                                                       15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-SEP-2003 (Rel. 36, Last amontation update)
Exostosin-like 1 (EC 2.4.1.224) (Glucuronosyl-N-acetylglucosaminyl-protecylcyan 4-alpha-N-acetylglucosaminyltransferase) (Exostosin-L)
EXTL OR EXTL.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                  23 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRF 53
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                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human)
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SEQUENCE FROM N.A.
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MIM, 601738; ...
GO: GO:0008181; F:tumor suppressor; TAS.
GO: GO:0001501; F:skeletal development; TAS.
InterPro; IPR004263; Exostosin.
Fransferase; Glycostosin; I.
Transferase; Glycosyltransferase; Endoplasmic reticulum;
Transmembrane; Signal-anchor; Glycoprotain; Polymorphism.
TORNEMENT 1 9 CYTOPLASMIC (POTENTIAL).
DOWNIN 1 0 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus (Rat).
Rukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
NCBI_TaxID=10116;
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                                                                                                                                                                                                                                                      LUMENAL (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
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TISSUB-Test18;

MEDLINE-90370473; PubMed=2204029;

MEDLINE-90370473; Pactucci R., Pellicer A.;

"Characterization of unr; a gene closely linked to N-ras.";

Nucleic Acida Res. 18:4891-4899(1990).

-I - FUNCTION: RNA-BINNING PROTEIN (BY SIMILARITY).

-I - SUBCELLULAR LOCATION: Cytoplesmic.

-I - SIMILARITY: BELONGS TO THE COLD-SHOCK DOMAIN (CSD) PAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                29.9%; Score 46; DB 1; Length 676; 45.0%; Pred. No. 12; tive 3; Mismatches 8; Indels
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/FTId=VAR 012830.
676 AA; 74673 MM; B5E006A8762E5633 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          798 AA.
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PIR; S11210; S11210.
HSSP; P15277; IN20.
Interpro; IRR002059; Cold_shock.
Pfam; PP00313; CSD; 7.
ProDom; PD00621; Cold_shock; 1.
SMART; SM00357; CSP; 5.
PROSITE; PS00352; COLD_SHOCK; 4.
RNA-binding; Repeat.
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269
379
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269
379
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01-NOV-1990
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CARBOHYD
VARIANT
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Gaps

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388 Potential. 47916 MW; 418B34F3245A8F21 CRC64;

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Similarity 29.6%; Score 45; DB 1; Length 428; Similarity 29.6%; Pred. No. 11; 8; Conservative 6; Mismatches 13; Indels
                                                                                        2 RXHXHSMEXRTPDINPAWYXXRGIRPV 28
           428 AA;
                                Query Match
Best Local Similarity
Matches 8; Conserv
ACT SITE
SEQUENCE
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                                                                                                                                           PLSC_HELPY
                                                                                                                                 RESULT
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                                                                  ö
                                                                                                                                                                                      (Rel. 41, Created)
(Rel. 41, Last sequence update)
(Rel. 41, Last annotation update)
(EC 3.2.1.18) (Membrane sialidase) (Ganglioside sialidase)
                                                                                                                                                                                                                                                                                                                                                                                                                                         -1- CATALYTIC ACTIVITY: Hydrolygis of alpha-(2->3)-, alpha-(2->6)-, alpha-(2->6)-, alpha-(2->8)-glycosidic linkages of terminal sialic residues in oligosaccharides, glycoproteins, glycolipids, colominic acid and synthetic substrates.
-1- SUBCELLULAR LOCATION: Membrane-associated (By similarity).
-1- TISSUE SPECIFICITY: Expressed in brain.
-1- SIMILARITY: BELONGS TO PAMILY 33 OF GLYCOSYL HYDROLASES.
                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                      ŝ
                                                                                                                                                                                                                                                                                                                                                                         "Molecular cloning and characterization of a plasma membrane-associated stalldase specific for gangliosides.";
J. Biol. Chem. 274:5004-5011(1999).
-1- FUNCTION: Plays at content of the level of membrane-bound sialyl
                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
                                                                                                                                                                                                                                                                                                                                          MEDLINE=99141165; PubMed=9988745;
Miyagi T., Wada T., Iwamatsu A., Hata K., Yoshikawa Y., Tokuyama
Sawada M.;
                                                                  ö
                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., PARTIAL SEQUENCE, AND CHARACTERIZATION
                                         Score 46; DB 1; Length 798;
Pred. No. 14;
4; Mismatches 10; Indels
                      F484B3FA8B0995A4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Potential.
Potential.
By similarity.
Potential.
                                                                                                                                                                  428 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Glycosidase; Membrane; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BNR 3.
FRIP MOTIF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Potential.
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 CSD 8.
                                                                                      6 HSMEXRTPDINPAWYXXRGIRPV 28
                                                                                                                                                                                                                                (N-acetyl-alpha-neuraminidase 3).
           735 C
88894 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AB008184; BAA75071.1;
Interpro; IPR002860; GH_BNR.
Pfam; PF02012; BNR; 3.
Hydrolase; Glycosidase; Memb
                                            29.98;
                                                     39.1%;
                                                     Best Local Similarity 39.1
Matches 9; Conservative
                                                                                                                                                                 STANDARD;
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272
272
273
273
273
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274
374
11
                                                                                                                                                                                                                                                                                        Bovidae, Bovinae, Bos.
                                                                                                                                                                                                                                                      Bos taurus (Bovine).
  610
674
798 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                  glycoconjugates
                                                                                                                                                                                                                                                                                              NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        203
254
24
25
                                                                                                                                                                                                                                                                                                                                   TISSUE=Brain;
                                                                                                                                                                                      28-PEB-2003
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                                                                                                                                                                                                            28-FEB-2003
                                                                                                                                                                                                                        Sialidase 3
                                                                                                                                          RESULT 6
NER3 BOVIN
ID NER3 BOVIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIR=26595 / ATCC 700392;
MEDLINE=26595 / ATCC 700392;
Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,
Tomb J.-F., White D., Kerchum K.A., Klenk H.-F., Gill S., Dougherty B.A.,
Nelson K., Quackenbush J., Zhou L., Kirkness B.P., Peterson S.,
Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A.,
McKenney K., FitzGerald L.M., Lee N., Adams M.D., Hickey B.K.,
Cotton M.D., Weidman J.M., Fujii C., Bowman C., Watthey L., Wallin B.,
Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -1- FUNCTION: CONVERTS LYSOPHOSPHATIDIC ACID (LPA) INTO PHOSPHATIDIC ACID BY INCORPORATING ACYL MOISTY AT THE 2 POSITION.
-1- CATALYTIC ACITVITY: ACYL-CA + 1-acyl-mglycerol 3-phosphate = CoA + 1,2-diacyl-sn-glycerol 3-phosphate.
-1- PATHWAY: De novo phospholipid biosynthesis; second step.
-1- SUBCRILIDIAR LOCATION: Inner membrane-associated (Potential).
-1- SIMILARITY: BELONGS TO THE 1-ACYL-SN-GLYCEROL-3-PHOSPHATE
ACYLTRANSPERASE PAMILY.
                                                                                                                                                                                                 1-acyl-sn-glycerol-3-phosphate acyltransferase (BC 2.3.1.51) (1-AGP acyltransferase) (1-AGPAT) (Lysophosphatidic acid acyltransferase)
                                                                                                                                                                                                                                                                                                                                                      Helicobacter pylori (Campylobacter pylori).
Bacteria, Proteobacteria, Epsilonproteobacteria, Campylobacterales,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The complete genome sequence of the gastric pathogen Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 240;
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InterPro; IPR004552; AGP acyltrn.
Pfan; PR01553; Acyltransferase; 1.
SMART; SM00563; PlsC; 1.
TIGRPAMs; TIGR00530; AGP acyltrn; 1.
Phospholipid blosynthesië; Transferase; Acyltransferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22BD5D0EB190BBDD CRC64;
                                                                      15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
    240 AA
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    PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Helicobacteraceae, Helicobacter
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 388:539-547(1997)
    STANDARD;
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PLSC_HELPY
025903;
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UVRA METTH
O26543;
30-MAY-2000
30-MAY-2000
  sialidase.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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(Rel. 41, Last annotation update)
(RC 3.2.1.18) (Membrane sialidase) (Ganglioside sialidase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wada T., Yoshikawa Y., Tokuyama S., Kuwabara M., Akita H., Miyagi T., "Cloning, expression, and chromosomal mapping of a human ganglioside
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                       Gaps
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-1- SIMILARITY: BELONGS TO THE FRUCTOSAMINE KINASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Pasteurella.
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InterPro; IPR005581; Pructosamin kin.
Pfam; PF03881; Pructosamin kin; I.
Hypothetial protein; Transferse; Kinase; Complete proteome.
SEQUENCE 288 AA; 33778 MM; P4D2F6C26014D940 CRC64;
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                       Indels
                       6
                                                                                                                                                                                                                                               (Rel. 40, Created)
(Rel. 40, Last sequence update)
(Rel. 40, Last annotation update)
                                                                                                                                                                                                           288 AA
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Best Local Similarity 42.9%; Pred. No. 7;
Matches 9; Conservative 2; Mismatches
                                                                                                                                                                                                         PRT;
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                                                                                            197 ARTRIVMLESYTPDFNSPTWY 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=21145866; PubMed=11248100;
                                                            1 SRXHXHSMEXRIPDIN-PAWY 20
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Q9UQ49; Q9NQE1;
28-FEB-2003 (Rel. 41, Created)
                                                                                                                                                                                                                                                                                                              Hypothetical protein PM0587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8; Conservative
                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                         Pasteurella multocida.
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TISSUE=Brain;
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                                                                                                                                                                                                                                               16-OCT-2001
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16-OCT-2001
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Q9CN56;
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                                                                                                                      Monti E., Bassi M.T., Papini N., Riboni M., Manzoni M., Venerando B., Croci G., Prett A., Ballabio A., Tettamanti G., Borsani G.; aldentification and expression of NEU3, a novel human sialidase associated to the plasma membrane."; Biochem. J. 489:343-351(2000).

-!- FUNCTION: Plays a role in modulating the ganglioside content of the lipid bilayer at the level of membrane-bound sialyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                        glycoconjugates.
CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-,
alpha-(2->8)-glycosidic linkages of terminal sialic residues in
oligosaccharides, glycoproteins, glycolipids, colominic acid and
synthetic substrates.
                                                                                                                                                                                                                                                                                                                                                                                                                                   -i- SÜBÜELLÜLAR LÖCATION: Membrane-associated.
-i- TISSUB SPECIFICITY: Highly expressed in skeletal muscle, testis, adrenal gland and thymus, followed by pancreas, liver, heart and thymus. Weakly expressed in kidney, placenta, brain and lung.
-i- MISCELLANEOUS: Optimum pH is 3.8.
-i- SIMILARITY: BELONGS TO FAMILY 33 OF GLYCOSYL HYDROLASES.
-i- SIMILARITY: Contains 3 BNR repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               35D1DD9359A78C98 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MIM; 604617; -.
GO; GO:0005887; C:integral to plasma membrane; TAS.
GO; GO:0005889; P:ganglioside catabolism; TAS.
InterPro; IPR002860; GH_BNR.
Pfam; PF02012; BNR; 3.
Hydrolase; Glycosidase; Membrane; Repeat.
Biochem. Biophys. Res. Commun. 261:21-27(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          962 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Potential.
By similarity.
Potential.
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(Rel. 39, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  By similarity. Potential.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 15; 5; Mismatches
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199 HSLMIYSDDLGVTWHHGRLIRPM 221
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BNR 2.
BNR 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AB008185; BAA82611.1; -.
EMBL; Y18563; CAB96131.1; ALT_INIT.
Genew; HGNC:7760; NEU3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 HSMEXRTPDINPAWYXXRGIRPV 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                           SEQUENCE FROM N.A.
TISSUE-Skeletal muscle;
PubMed=10861246;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22140
22140
22140
22140
2212
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340
370
387
428 AA;
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-1- SUBCELLUIAR LOCATION: Integral membrane protein.
-1- TISSUB SPECIFICITY: LATERAL BYE.
-1- PTM: SOME OR ALL OF THE CARBOXYL-TERMINAL SER OR THR RESIDUES MAY BE PHOSPHORYLATED (BY SIMILARITY).
-1- MISCELLANBOUS: THIS OPSIN HAS AN ABSORPTION MAXIMUM AT 520 NM.
-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                            Lateral eye opsin.
Limulus polyphemus (Atlantic horseshoe crab).
Bukaryota, Metazoa, Arthropoda, Chelicerata, Merostomata, Xiphosura,
Limulidae, Limulus.
                                                                                                                                                                                                 TISSUB-Lateral eye;
MEDLINE-93317641; PubMed=8327495;
Smith W.C., Price D.D., Greenberg R.M., Battelle B.-A.;
"Opains from the lateral eyes and ocelli of the horseshoe crab,
(Rel. 29, Created)
(Rel. 29, Last sequence update)
(Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  46
710
833
1123
1143
1162
74
74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             193
376 AA;
                                                                                                                                                                                 SEQUENCE PROM N.A.
                                                                                                                                            NCBI_TaxID=6850;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CARBOHYD
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TRANSMEM
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TRANSMEM
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      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its meeb by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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7
                                                                                                                                                                                                                  Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois J., Andreege T., Bashizzadeh R., Blakely D., Cook R., Gilbert K., Andreege T., Bashizzadeh R., Blakely D., Cook R., Gilbert K., Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D., Spadafora R., Vicare R., Wang Y., Waerzbowski J., Gibson R., Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S., Anfourgali S., Shimer G., Goyal A., Pietrovski S., Church G.M., Daniels C.J., Mao J.-I., Robelling J., Reeve J.N., T., Complete genome sequence of Methanobacterium thermoautotrophicum T. deltem: functional analysis and comparative genomics."; J. Bacteriol. 179:135-7155 (1997).

I. FUNCTION: The UvraBc repair system catalyzes the recognition and processing of DNA legions. Uvra is an ATPase and a DNA-binding processing of DNA legions. Uvra is an ATPase and a DNA-binding processing of DNA legions. Uvra is an ATPase and a DNA-binding current and an antiles scans DNA for abnormalities. When the presence of a lesion has been verified by uvrB, the uvra molecules dissociate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (By similarity).
SUBUNIT: Forms a heterotetramer with uvrB during the search for lesions (By similarity).
SUBCELULAR LOCATION: Cytoplasmic (By similarity).
SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. UVRA SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PEAM; PP00005; ABC_tran; 2.
ProDom; PD00006; ABC_transporter; 1.
ProDom; PT000006; ABC_transporter; 1.
TIGRFAMS; TIGR00630; uvra; 1.
PROSITE; PS00211; ABC_TRANSPORTER_1; 2.
PROSITE; PS0093; ABC_TRANSPORTER_2; 2.
PROSITE; PS00993; ABC_TRANSPORTER_2; DAA repair; DNA recombination; DNA excision; ATF-binding; DNA repair; Zinc; Metal-binding;
                      UvrABC system protein A (UvrA protein) (Excinuclease ABC subunit A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18;
                                                                              Archaea; Buryarchaeota; Methanobacteria; Methanobacteriales;
Methanobacteriaceae; Methanothermobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28.6%; Score 44; DB 1; Length 962; 36.8%; Pred. No. 35; tive 0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                748 774 C4-TYPE.
962 AA; 108395 MW; 2C0EF7FC41CCD060 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               703 RIPRSNPATYTGVFTHIRELFAQTPEARKRGYRP-GRF 739
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      28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATP (POTENTIAL)
ATP (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AE000828; AAB84949.1; -.
PIR; H69157; H69157.
HAMAP; MP 00205; -; 1.
InterPro; IPR003593; AAA_ATPASE.
InterPro; IPR003439; ABC_transporter.
InterPro; IPR004602; UvrĀ.
                                                             Methanobacterium thermoautotrophicum,
                                                                                                                                                                                 STRAIN=Delta H;
MEDLINE=98037514; PubMed=9371463;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zinc-finger; Complete profeome.
NP BIND 45 AT
NP BIND 636 AT
ZN_FING 748 774 C4
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                                                                                                                     NCBI_TaxID=187420;
                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 11
OPS1_LIMPO
ID OPS1_LIMPO
AC P35360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Photoreceptor; Retinal protein; Transmembrane; Glycoprotein; Vision; Phosphorylation; G-protein coupled receptor.

DOMAIN

1 46

EXTRACELLULAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RETINAL CHROMOPHORE (BY SIMILARITY)
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
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                                                                                                                                                                                        EMBL; L03791; AAA28273.1; -
EMBL; L03781; AAA2498.1; -
PIR; B40897; B40897.
HSSP; P02699; 1EDV.
INTEPPO; IPR00176; GPCR Rhodpen.
INTEPPO; IPR00176; OPBIN.
FAM; PP00001; 7rm 1; 1.
PRINTS; PR00237; GPCRHODDSN.
PROSITR; PS00237; GPROTEIN RECEP_F1; 1.
PROSITR; PS00237; GPROTEIN RECEP_F1; 1.
PROSITR; PS00237; GPROTEIN RECEP_F1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S (POTENTIAL).
CYTOPLASMIC.
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CYTOPLASMIC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 (POTENTIAL).
EXTRACELLULAR.
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EXTRACELLULAR
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CYTOPLASMIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (POTENTIAL)
CYTOPLASMIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 43; DB
Pred. No. 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 (POTENTIAL)
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Best Local Similarity
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Matches
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STANDARD;

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CYCR CHRVI
082947;
BINDING
CARBOHYD
CARBOHYD
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    METAL
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                                                                                                                                                        CYCR_CHRVI
                                                                      Matches
                                                                                                                                               RESULT 13
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                                                                                                                                                                                                                                                                                           -1- SUBCELLULAR LOCATION: Integral membrane protein.
-1- TISSUB SPECIFICITY: OCELLAR CELLS; MEDIAN OCELLI.
-1- PTM: SOME OR ALL OF THE CARBOXTL-TERMINAL SER OR THR RESIDUES MAY
BE PHOSPHORYLATED (BY SIMILARITY).
-1- MISCELLANEOUS: THIS OPSIN HAS AN ABSORPTION MAXIMUM AT 530 NM.
-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                          Limulus polyphemus.";
Proc. Natl. Acad. Sci. U.S.A. 90:6150-6154 (1993).
--- FUNCTION: VISUAL PIGMENTS ARE THE LIGHT-ABSORBING MOLECULES THAT MEDIATE VISION. THEY CONSIST OF AN APOPROTEIN, OPSIN, COVALENTLY LINKED TO CIS-RETINAL.
                                                                                                                                  Limulus polyphemus (Atlantic horseshoe crab).
Bukaryota; Metazoa; Arthropoda; Chelicerata; Merostomata; Xiphosura;
Limulidae; Limulus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Glycoprotein; Vision;
                                                                                                                                                                                                 TISSUE-Median ocelli;
MEDLINE-93317641; PubMed-8327495;
Smith W.C., Price D.A., Greenberg R.M., Battelle B.-A.;
"Opsins from the lateral eyes and ocelli of the horseshoe crab,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Photoreceptor; Retinal protein; Transmembrane;
                                                                                           01-JUN-1994 (Rel. 29, Created)
101-JUN-1994 (Rel. 29, Last sequence update)
101-CTT-2001 (Rel. 40, Last annotation update)
Ocellar opsin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL, L03792; AAA28274.1; --
EMBL, L03782; AAA02499.1; --
PIR, A48197; --
HSP: P02699; LBD'.
InterPro; IPR000276; GPCR_Rhodpsn.
InterPro; IPR001760; Opain.
PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; GPCRHODOPSN.
PROSITE; PS00237; GPROTEIN RECRP_F1.1; 1.
PROSITE; PS00238; OPSIN; 1.
                                                                        376 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          G-protein coupled receptor 46 EXTRACELLULAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CYTOPLASMIC.
2 (POTENTIAL).
EXTRACELLULAR.
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CYTOPLASMIC.
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EXTRACELLULAR.
7 (POTENTIAL).
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CYTOPLASMIC.
BY SIMILARITY.
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EXTRACELLULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (POTENTIAL)
                                                                        PRT;
             40 PPMNPLWYSILGV-52
 13 PDINPAWYXXRGI 25
                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                            OPSIN SUBFAMILY.
                                                                                                                                                                              [1]
SEOUENCE PROM N.A.
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DOMAIN
                                                                                                                                                                    NCBI_TaxID=6850;
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144
163
187
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TRANSMEM
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                                                                                   P35361;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AB011811; BAA32742.1; -.
HSSP; P0173; 6PRC.
InterPro; IPR000345; CytC_Reme_bind.
InterPro; IPR0003158; CytC_RC.
Prodom; P010011; CytC_RC; 1.
Prodom; P010011; CytC_RC; 1.
PROSITE; P800130; CytCTGCROME C; 4.
Electron transport; Photosynthesis; Reaction center; Heme; Membrane; Lipoprotein; Repeat; Signal.
Signal.
23 PHOTOSYNTHERITY.
CHAIN 23 383 PHOTOSYNTHERITY REACTION CENTER CYTOCHROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OXIDIZED PRIMARY ELECTRON DONOR.

-!- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor (By similarity).

-!- PTM: BINDS FOUR HEME GROUPS PER MOLECULE.

-!- SIMILARITY: HIGH, WITH OTHER PHOTOSYNTHETIC REACTION CENTER CYTOCHROME C SUBUNITS.
                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

STRAIN=D / ATCC 17899 / DSM 180;

COTSON G.E., Nagashima K.V., Matsuura K., Sakuragi Y., Ruwanthi W.,

COTSON G.E., Allen R., Knaff D.B.;

"Primary structure of genes encoding light-harvesting and reaction
center protedins from Chromatium vinosum.";

Submitted (MAR-1998) to the RMBL/GenBank/DDBJ databases.

Submitted (MAR-1998) to The RMBL/GenBank/DDBJ databases.

TIGHTLY BOUND CYTOCHROME MOLECULE WHICH RE-REDUCES THB PHOTO
  RETINAL CHROMOPHORE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N. ACYL DIGLYCERIDE (BY SIMILARITY).
IRON (HEME 1 AXIAL LIGAND)
(BY SIMILARITY).
HEME 1 (COVALENT) (BY SIMILARITY).
HEME 1 (COVALENT) (BY SIMILARITY).
IRON (HEME 1 AXIAL LIGAND)
(BY SIMILARITY).
IRON (HEME 2 AXIAL LIGAND)
(BY SIMILARITY).
                 17 N-LINKED (GLCNAC. .) (POTENTIAL)
193 N-LINKED (GLCNAC. .) (POTENTIAL)
42111 MW, PA9647C40531CBF8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (BY SIMILARITY)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-MAY-2000 (Rel. 39, Last sequence update)
15-8EP-2003 (Rel. 42, Last annotation update)
Photosynthetic reaction center cytochrome C subunit precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chromatium vinosum.
Bacteria; Proteobacteria; Gammaproteobacteria; Chromatiales;
                                                                                                                                   27.9%; Score 43; DB 1; Length 376; 46.2%; Pred. No. 19;
                                                                                                                                                                                             5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                     383 AA.
                                                                                                                                                                                             2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C SUBUNIT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chromatlaceae; Allochromatium.
NCBI_TaxID=1049;
                                                                                                                                                                                                                                                    PDINPAWYXXRGI 25
                                                                                                                                                                                                                                                                                       40 PPMNPLWYSILGV 52
                                                                                                                                                                                                6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23
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318 3
17
193 1
376 AA;
                                                                                                                                      Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=KIZ. / MG1655,
MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997).
-1- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yura T., Mori H., Nagai H., Nagata T., Ishihama A., Fujita N., Isono K., Mizobuchi K., Nakata A.; Systematic sequencing of the Escherichia coli genome: analysis the 0-2.4 min region...; Nucleic Acids Res. 20:3305-3308(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Potential).
-!- SIMILARITY: BELONGS TO THE SODIUM:ALANINE SYMPORTER FAMILY (SAF). STRONG, TO H.INPLUENZAE H10183.
                                                                                                                                                                                                                                                                        ö
                                                                                                                                              (BY SIMILARITY).
HEMB 4 (COVALENT) (BY SIMILARITY)
HEMB 4 (COVALENT) (BY SIMILARITY)
IRON (HEME 4 AXIAL LIGAND)
                         (BY SIMILARITY)
(BY SIMILARITY)
                                                                                                         (BY SIMILARITY)
(BY SIMILARITY)
                                                                                                                                                                                                                                          Score 43; DB 1; Length 383;
Pred. No. 20;
3; Mismatches 9; Indels
                                                                                                       HEME 3 (COVALENT) (BY SIMI)
HEME 3 (COVALENT) (BY SIMI
IRON (HEME 3 AXIAL LIGAND)
                                                                 (BY SIMILARITY).
IRON (HEME 3 AXIAL LIGAND)
(BY SIMILARITY).
                                                      (HEME 2 AXIAL LIGAND)
 RON (HEMB 4 AXIAL LIGAND)
                                                                                                                                                                                                                  96BCD91FF1B9AE7E CRC64;
                                       (COVALENT)
                                                                                                                                                                                                                                                                                                                                                                                                                    01-UUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last gequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Putative transporter yaaJ.
                                                                                                                                                                                                                                                                                                                                                                                                 476 AA
                                                                                                                                                                                                     (BY SIMILARITY)
              BY SIMILARITY
                         HEME 2
HEME 2
IRON (H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=92334977; PubMed=1630901;
                                                                                                                                                                                                                                                                                                                   263 TPORTTAWYAIRHVRDING 281
                                                                                                                                                                                                                                                                                                   12 TPDINPAWYXXRGIRPVGR 30
                                                                                                                                                                                                                    41522 MW;
                                                                                                                                                                                                                                             27.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; D10483; BAB96585.1; -.
                                                                                                                                                                                                                                                         Local Similarity 36.8
                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
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155
156
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250
251
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                                                                                                                                                                                                                     383 AA;
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                                                                                                                       250
                                                                                                                                                               307
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P30143;
                                                                                                                                                                                                                  SEQUENCE
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                                                                                                                                                            BINDING
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                         BINDING
                                       BINDING
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YAAJ_ECOLI
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METAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Pol polyprotein [Contains: Protease (RC 3.4.23.-); Reverse transcriptase (RC 2.7.7.49); Ribonuclease H (RC 3.1.26.4)] (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Determinants of thymotropism in Kaplan radiation leukemia virus and nucleotide sequence of its envelope region.";
J. Virol. 66:5141-5146(1992).
-!- CATALYTIC ACTIVITY: Endonucleolytic cleavage to 5'-
                                                                                                                                                                                                                                                                                                                                                                                Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    + {DNA}(N).
--- PTM: SPECIFIC ENZYMATIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS.
--- MISCELLANEOUS: THIS PROTEIN IS SYNTHESIZED AS A GAG-POL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE=92333703; PubMed=1629969;
Poliquin L., Bergeron D., Fortler J.L., Paquette Y., Bergeron R.,
EMBL; AE000111; AAC73118.1; -.

PIR; G64720; G64720.

BccGene; EG11555; yaa.

InterPro; IPR002293; AA/rel_permeasel.

InterPro; IPR00463; Na/Ala_symport.

PRINTS; PR0175; NaALASMPORT.

TIGREAMS; TIGR06835; agc.5; 1.

PROSITE; PS06835; adc.5; 1.

PROSITE; PS06831; AA ALANINE SYMD; 1.

Hypothetical protein; Transmembrane; Inner membrane; Transport;
                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                                               Score 43; DB 1; Length 476;
Pred. No. 25;
                                                                                                                                                                                                                                                                                                                                                                                IndelB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Radiation murine leukemia virus (strain Kaplan).
Viruses; Retroid viruses; Retroviridae; Gammaretrovirus.
NCBI_TaxID=31689;
                                                                                                                                                                                                                                                                                                      POTENTIAL.
2P6BB2B12B126B63 CRC64;
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120 DVNGQFRGGPAWYMARGL 137
                                                                                                                                                                                                                                                                                                                                                                                                          14 DIN-----PAWYXXRGI 25
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                                                                                                                                                                                                                                                                                                                      51662
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hes 8, Conservative
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HSSP; P29253; 1RIL.
                                                                                                                                                                                                                                                                                                      414
476 AA;
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P31795;
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Matches
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POL MLVRK
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DR MEROPS; A02.008; -.

DR InterPro; IPR001569; RadseH.

DR InterPro; IPR001564; RadseH.

DR InterPro; IPR001564; RadseH.

DR InterPro; IPR001564; RadseH.

DR Pfam; PP00675; rnaseH; 1.

DR PFGM; PP00675; rnaseH; 1.

DR PGM; PP00675; rnaseH; 1.

CM Hydrolase; Transferase; RNA-directed DNA polymerase;

KW Aspartyl protease; Endonuclease; Polyprotein.

FT NOW TER 1

SQ SEQUENCE 581 AA; 65157 MW; 8D7A38694C8R036E CRC64;

QUery Match

Guery Match

Best Local Similarity 34.84; Pred. No. 30;

Matches 8; Conservative 2; Mismatches 13; Indels 0; Gaps 0;
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Search completed: December 3, 2003, 19:12:03 Job time : 6.25 secs

6 HSMEXRTPDINDAMYXXRGIRPV 28

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Scoring table:

Searched:

Database

Sequence:

Run on:

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Q9ph76 xylella fas Q4541 caenorhabdi Q9da19 mus musculu O60087 homo sapien Q8ww85 homo sapien Q91gz0 oryza sativ Q813r1 mus musculu Q91x0 arabidopsis Q91x0 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9pd41 xylella fas
Q8rf10 fusobacteri
Q912f2 pseudomonas
O50128 pyrococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

Curlewis J.D., Kusters D.H.L., Barclay J.L., Anderson S.T.;

"Prolactin-releasing peptide (PrRP) in the ewe: cDNA cloning, mRNA distribution and effects on prolactin secretion in vitro and in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ovis aries (Sheep).

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidae, Caprinae, Ovis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94.8%; Score 146; DB 6; Length 98; 83.9%; Pred. No. 7.8e-16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases EMBL; AF450453; AAL47178.1; -. SEQUENCE 98 AA; 10513 MW; 2A53331ED62CAAB5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-WAR-2002 (TrEMBLrel. 20, Created)
01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
01-WAR-2002 (TrEMBLrel. 20, Last annotation update)
Preproprolactin-releasing peptide.
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Q8KZ57
Q9ZGE5
Q8P0K1
Q9RSN5
                                        Q9DA19
O60687
Q8WW85
Q9LGZ0
Q8R3R1
Q8JZN2
Q9JW50
                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9KGP0
Q9EYB3
Q95ZB5
                                                                                                                                                                                                                                                                                                               Q9A5E9
Q20170
Q8ZXH2
Q8FM04
Q8BJI9
Q8BJI9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                 OSLYX0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
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(TrEMBLrel. 19,
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hes 26; Conservative
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      Q9W624
Q9W624;
01-NOV-1999 (
01-NOV-1999 (
      23
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QBWN12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT : 09W624 ID 09W AC 09W DT 01L DT 01L DT DT 01L DT 01L DT 01L
      28WN12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               O9w624 carassius a Q918j6 rhodospiril Q9118j6 rhodospiril Q91022 pseudomonas Q91022 pseudomonas Q9m371 arabidopsis P74747 synechocyst Q97a00 thermoplasm Q8ktv7 uncultured Q9kb39 chlorobium Q8k746 streptococc Q931z7 streptomyce Q9kb39 mycobacteri Q08km3 agrobacteri O06348 mycobacteri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q8wn12 ovis aries
                                                                                                                                     3, 2003, 19:03:25; Search time 26.5 Seconds (without alignments) 301.873 Million cell updates/sec
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                        GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                          1 SRXHXHSMEXRTPDINPAWYXXRGIRPVGRF 31
                                                                                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                       830525 seqs, 258052604 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                   OM protein - protein search, using sw model
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Q9M624
Q9U846
Q911W4
Q91102
Q9N102
Q9N102
Q9N2A0
Q8R39
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1: Sp_archea:*
2: Sp_bacteria:*
3: Sp_fungi:*
4: Sp_fungi:*
5: Sp_invertebrate:*
5: Sp_mhc:*
5: Sp_mhc:*
6: Sp_phage:*
6: Sp_ph
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Gapop 10.0 , Gapext 0.5
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sp_unclassified:*
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sp_bacteriap:*
sp_archeap:*
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length: 2000000000
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154
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sp_virus:*
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STRAINB-ATCC 15692 / PRO1;
STRAINB-ATCC 15692 / PRO1;
STRAINB-20437337; PubMed=10984043;
SCOVET C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., Garber R.L., Goltry L., Tolentino B., Westbrock-Wadman S., Yuan Y., Brody L.L., Coulter S.M., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saler M.H., Hancock R.B.W., Lory S., Olson M.V.;
"Complete genome sequence of Pseudomonas aeruginosa PAO1, an Opportunistic pathogen.";
Nature 406:959-964(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

STRAIN=ATCC 15692 / PAO1;

STRAIN=ATCC 15692 / PAO1;

STRAIN=ATCC 15692 / PAO1;

STRAIN=ATCC 15692 / PAO1;

STOAT STRAIN=ATC 15692 / Branch A.L., Mizoguchi S.D., Warrener P., Stooter C.K., Pham X.-Q.T., Brwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman P.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., Garber R.L., Goltery L., Tolentino B., Westbrock-Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;

"Complete genome sequence of Pseudomonas aeruginosa PAO1, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
NCBI TaxID=287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                32.1%; Score 49.5; DB 16; Length 664; 62.5%; Pred. No. 22; 4; Indels 1; Mismatches 4; Indels 1:
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EMBL; AB004709; AAG06209.1; -.

Interpro; IPR004046; GST_Cterm.

Interpro; IRR004045; GST_Nterm.

Pfam; PP00043; GST_C; 1.

Pfam; PP02798; GST_N; 1.

Transferaes; Complete proteome.

SEQUENCE 220 AA; 24716 MW; 6596183RA6CAA050 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfan, PF00128; alpha-amylase; 1.
PR051TE; PS001019; ACTININ 1; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 664 AA; 76329 MW; 8F59FEED54C308AD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2001 (TrEMBLrel. 16, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30
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Q91022,
01-0042,
01-0042, TERMELrel. 16, Created)
01-0047, Created)
                                                                                                                                                                                                                                                                                                                                                                                             EMBL, AE004642, AAG05539.1, -.
InterPro, IPR001589, Actbind actnin.
InterPro, IPR006047, Alpha_amyl_cat.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Probable glutathione S-transferase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12 TPDINPAWYXXRGIRP 27
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Best Local Similarity 44.v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 32.1
Best Local Similarity 62.5
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             opportunistic pathogen.
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Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                      Carassius auratus (Goldfish).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Actinopterygii, Neopterygii; Teleostei; Ostariophysi; Cypriniformes,
Cyprinidae; Carassius.
NCBI_TaxID=7957;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cheng Y.S., Brantner C.A., Tsapin A., Collins M.L.P.;
"Role of the H protein in assembly of the photochemical reaction
enter and intracycoplasmic membrane in Rhodospirillum rubrum.";
J. Bacteriol. 182:120010-1207 (2000).

EMBL, AF202319; AAF37352.1;
EMBL, AF202319; AAF37352.1;
InterPro; IPR003672; CobN/Mg_chltase.
Pfam; PF02514; cobN-Mg_chel; 1.

NOW TER

SEQÜENCE 692 AA; 75453 MW; 96430AE93BF35680 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria, Proteobacteria, Alphaproteobacteria, Rhodospirillales,
Rhodospirillaceae, Rhodospirillum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pseudomonas aeruginosa.
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Indels
                                                                                                                                                                                                                                                                         Satake H., Minakata H., Fujimoto M.;
"Carassius RFamide (C-RF amide)";
submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; ABC10024; BAA76662.1; -
SEQUENCE 117 AA; 12879 WW; D5DC4CB22038C2B0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q911W4 PRELIMINARY, PRT, 664 AA. Q911W4; C1 PRELIMINARY, C1 PRT, 664 AA. Q911W4; C1 PREMELT 16, Created) 01-MAR-2001 (TrEMBLTE1: 16, Last sequence update) 01-MAR-2003 (TrEMBLTE1: 23, Last annotation update)
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                             63.6%; Score 98; DB 13;
53.8%; Pred. No. 5.1e-08;
ative 8; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          692 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |:| || :| || 572 SLETRTRALNPKWYEGMLAHGYEGVRQI 599
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6 HSMEXRTPDINPAWYXXRGIRPVGRF 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=R5;
MEDLINE=20138142; PubMed=10671438;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical protein PA2151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
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                                                                                                                                                                                                                SEQUENCE FROM N.A.
TISSUE=Brain;
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STRAIN-GSS1 / DSM 4299 / JCM 9571;
MEDLINE-20570466; PubMed-11121031;
MEDLINE-20570466; PubMed-11121031;
Kawashima T., Amano N., Kolke H., Makino S.-I., Higuchi S.,
Kawashima T., Amano N., Aramaki H., Makino K., Suzuki M.;
Nunoshiba T., Yamamoto Y., Aramaki H., Makino K., Suzuki M.;
"Archaeal adaptation to higher temperatures revealed by genomic sequence of Thermoplasma volcanium.";
Proc. Natl. Acad. Sci. US. A. 97:14257-14262 (2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-21822632; PubMed-11832943; Bejā O., Suzuki M.T., Heidelberg J.F., Nelson W.C., Preston C.M., Hamada T., Eisen J.A., Fraser C.M., DeLong B.F.; "Unsuspected diversity among marine aerobic anoxygenic phototrophs.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 17; Length 173;
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                                                                                                                                                                                                                                           Thermoplasma Volcanium.
Archaea; Buryarchaeota; Thermoplasmata; Thermoplasmatales;
Thermoplasmataceae; Thermoplasma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 415:630-633(2002).

EMBL, AR008919, AAL76369.1;
Interpro; IPR003672; CobN/Mg_chltase.

Pfam; PP02514; cobN, Mg_chel; 1.

SEQUENCE 1253 AA; 137586 MW; C98ABC010E261511 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     173 AA; 19041 MW; 1A750DDB821C7524 CRC64;
                                                                                                                                    (TrEMBLrel. 18, Last sequence update) (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; environmental samples
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT; 1253 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 SMEXRIPDINPAWYXX-----RGIRPV 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 47;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CobN/magnesium chelatase family protein.
EBAC000-65D09.24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 HSMEXRTPDINPAWYXXRGIRPVGR 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 YBFEGRVPDIDPSAYVSESATVIGK 27
                                                                                                         (TrEMBLrel. 18, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (TrEMBLrel. 21, Created)
(TrEMBLrel. 21, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001451; Hexapep_transf.
Pfam; PF00132; hexapep; 4.
                                                 PRT;
                                                                                                                                                                                         Perripyochelin binding protein. TV1010 OR TVG1032219.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (TrEMBLrel, 22,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             uncultured proteobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 32.0
hes 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                    PRELIMINARY;
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hes 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=153809;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Complete proteome
                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=50339;
                                               Q97A00
Q97A00;
01-OCT-2001 (
01-OCT-2001 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-2002 (
01-JUN-2002 (
01-OCT-2002 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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Q93SV4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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RESULT 8
                       OBRTV7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SO DE L'ARRENT COOR EN L'ARRENT COUR EN 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ઠે
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                                                                                                                                                                                                                                        Arabidopeis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE=97061201; PubMed=8905231;
MEDLINE=97061201; PubMed=8905231;
Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T.,
Hosouchi T., Mateuno A., Muraki A., Nakazaki N., Naruo K., Okumura S.
Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ô
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 49; DB 10; Length 790;
Pred. No. 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   De Haan M., Maarse A.C., Grivell L.A., Mewes H.W., Lemcke Mayer K.F.X., Quetier F., Salanoubat M.;
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EU Arabidopsis sequencing project;
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AL132959; CAB71097.1; -.
Hypothetical protein:
SEQUENCE 790 AA; 871376 MW; B222724B75690F30 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL, D90917; BAA18867.1; -.
Hypothetical protein; Complete proteome.
SEQUENCE 128 AA; 13481 MW; 4FF5B364C38396F6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synechocystis sp. (strain PCC 6803).
Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
NCBL_TaxID=1148;
                                                                                                                              01-0CT-2000 (TrEMBLrel. 15, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11 SPENNQSLDCSSPDPSRKMYQARLFSFGITPTG 43
                                                    790 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT; 128 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3, Mismatches
                                                                                                            Created)
                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         366 PPHNPRTYGSRGLQPHGRW 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13 PDINPAWYXXRGIRPVGRF 31
                                                                                                                                                                                      Hypothetical 87.4 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical protein slr0601.
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Local Similarity 47.4%;
es 9; Conservative 3
                                                                                                      01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15,
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                                                 PRÉLIMINARY;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=3702;
                                                                                                                                                                                                                         P15G16.60.
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P74747;
                                                                               Q9M371;
                                                    09M371
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PRELIMINARY;

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STRAIN=MGAS31S / Serotype M3;
MEDLINE=2213808; Pubmed=1212206;
MEDLINE=2213808; Pubmed=1212206;
Bares S.B., Sylva G.L., Barbian K.D., Lei B., Hoff J.S.,
Mammarella N.D., Liu M.-Y., Smoot J.C., Porcella S.P., Parkins L.D.,
Campbell D.S., Smith T.M., McCormick J.K., Leung D.Y.M.,
Schlitevert P.M., Musser J.M.;
Genome sequence of a serotype M3 strain of group A Streptococcus:
phage-encoded toxins, the high-virulence phenotype, and clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 16; Length 416;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptomyces aureofaciens.
Bacteria; Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 46.5; DB 2; Length 420;
Pred. No. 41;
1; Mismatches 3; Indels 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30.2%; Score 46.5; DB 16; Length 25.0%; Pred. No. 40; ive 7; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                           DLTD OR SPYM3_0991.
Streptococcus_pyogenes (serotype M3).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proc. Natl. Acad. Sci. U.S.A. 99:10078-10083(2002).
RWBL, AR014156, AAW19598.1; -.
Complete proteome; Hypothetical
SEQUENCE 416 AA, 48086 MW; 876715258013E45A CRC64;
                                                                                                                                                                 01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Putative secreted protein DltD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 106 SLSHYYGMQQITNEMQKKKAIPVVSPQWFTAQGINP 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 SRXHXHSMEXRTPD-----INPAWYXXRGIRP 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       420 AA
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                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ||:
37 AWWAAVLRGESGIRPVGRF 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18 AWYXX-----RGIRPVGRF 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10; Conservative
                                                                                     PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=198466;
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01-OCT-2002 (
01-OCT-2002 (
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SEQUENCE FROM N.A.

STARIN=TLS / ATCC 46652 / DSM 12025;

K MEDLINE=22103685; PubMed=1203901;

A Eisen J.A., Nelson K.E., Paulsen I.T., Heidelberg J.P., Wu M.,

Bisen J.A., Nelson R.J., Paulsen I.T., Heidelberg J.P., Wu M.,

A Hickey E.K., Peterson J.D., Durkin A.S., Kolonay J.L., Yang F.,

A Holt I., Umayam L.A., Magon T., Brenner M., Shea T.P., Parksey D.,

Nierman W.C., Feldblyum T.V., Hansen C.L., Craven M.B., Radune D.,

Nierman W.C., Tettelin H., White O., Gluber T.M., Ketchum K.A.,

The complete genome sequence of Chlorobium tepidum TLS, a

Photosynthetic, anaerobic, green-sulfur bacterium.;

Proc. Natl. Acad. Sci. U.S.A. 99:9509-9514(2002).
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MEDLINE-20433268; PubMed=10976061;
Molecular Flacher W.M., Inoue K., Nakahara M., Bauer C.E.;
"Molecular evidence for the early evolution of photosynthesis.";
Science 289:174-1730 (2000)
EMBL, AX005136; AAG12412.1;
InterPro; IPR003672; CobM/Mg_chltase.
PFOS514; cobM-Mg_chel, T52C9D216549A2B1 CRC64;
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                                                                                                                                                                                                                                                                                     Chlorobium tepidum.
Bacteria; Chlorobi; Chlorobia; Chlorobiales; Chlorobiaceae;
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Bacteria; Chlorobi; Chlorobia; Chlorobiales; Chlorobiaceae;
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Pfam; PP02514; CobN-Mg_chel; 1.
Transferase; Methyltransferase; Complete protecme.
SEQUENCE 1278 AA; 142814 MW; 7983FB019A52AE22 CRC64;
                                        Created)
Last sequence update)
Last annotation update)
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BCHH-1 OR CT1957.
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01-OCT-2002 (TrEMBLrel. 22, Last seq
                                        01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, 01-JUN-2002 (TrEMBLrel. 21,
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Best Local Similarity 32.1.
Best Local 9; Conservative
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Q93SV4;
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MEDLINE=21608550; PubMed=11743193;

MEDLINE=21608550; PubMed=11743193;

MOOD D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,

Mood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,

Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,

A Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,

Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,

A Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,

Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.,

A Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.,

A Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,

Chumley P., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,

A Nester E.W.;

The genome of the natural genetic engineer Agrobacterium tumefaciens

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Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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NCBI_TaxID=176299;
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Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases
EMBL; AL035608; CAB55682.1;
NON_TER 54 5.4
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EMBL, AE008932; AL445769.1, -.
Hypoth AE108932 | Drotein; Plasmid; Complete proteome.
SEQUENCE 118 AA, 13099 MW; BE71C7BF8154CF5 CRC64;
                                                                  01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DJ479J7.3 (Sushi-repeat protein (SRPUL)) (Fragment)
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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                                   PRELIMINARY;
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Search completed: December 3, 2003, 19:14:02 Job time : 26.5 secs